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(54) A Method of identifying unknown adeno-associated virus (AVV) sequences and a kit for the method

Verfahren zur Identifizierung von Adeno-assoziiertem Virus (AAV) Sequenzen sowie Kit zur Ausführung der Methode

Une méthode d'identification de séquences de virus adéno-associés et kit permettant d'appliquer la méthode

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#### Description

### BACKGROUND OF THE INVENTION

[0001] Adeno-associated virus (AAV), a member of the Parvovirus family, is a small nonenveloped, icosahedral virus with single-stranded linear DNA genomes of 4.7 kilobases (kb) to 6 kb. AAV is assigned to the genus, Dependovirus, because the virus was discovered as a contaminant in purified adenovirus stocks. AAV's life cycle includes a latent phase at which AAV genomes, after infection, are site specifically integrated into host chromosomes and an infectious phase in which, following either adenovirus or herpes simplex virus infection, the integrated genomes are subsequently rescued, replicated, and packaged into infectious viruses. The properties of non-pathogenicity, broad host range of infectivity, including non-dividing cells, and potential site-specific chromosomal integration make AAV an attractive tool for gene transfer.

[0002] Recent studies suggest that AAV vectors may be the preferred vehicle for gene therapy. To date, there have been 6-different serotypes of AAVs isolated from human or non-human primates (NHP) and well characterized. Among them, human serotype 2 is the first AAV that was developed as a gene transfer vector; it has been widely used for efficient gene transfer experiments in different target tissues and animal models. Gene therapy vectors based on adeno-associated virus type 1 have also been disclosed (Xiao et al. J. Virology; May 1999; pages 3994-4008). Clinical trials of the experimental application of AAV2 based vectors to some human disease models are in progress, and include such diseases as cystic fibrosis and hemophilia B.

[0003] A general PCR method suitable for detecting human papillomavirus types in cutaneous tumours and normal skin is known (Forslund et al J. of General Virology: 1999 80: P2437-2443).

[0004] What are desirable are AAV-based constructs for gene delivery.

### SUMMARY OF THE INVENTION

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[0005] In one aspect, the invention provides a novel method of identifying unknown AAV sequences from cellular DNAs of various human and non-human primate (NHP) tissues using bioinformatics analysis, PCR based gene amplification and cloning technology, based on the nature of latency and integration of AAVs in the absence of helper virus co-infection, the method being defined in claim 1 hereinafter.

[0006] In another aspect the invention provides a kit for use in the method of the invention, the kit being as defined in claim 23 hereinafter.

### DETAILED DESCRIPTION OF THE INVENTION

[0007] In the present invention, the inventors have found a method which takes advantage of the ability of adeno-associated virus (AAV) to penetrate the nucleus, and, in the absence of a helper virus co-infection, to integrate into cellular DNA and establish a latent infection. This method utilizes a polymerase chain reaction (PCR)-based strategy for detection, identification of sequences of AAVs from DNAs from tissues of human and non-human primate origin as well as from other sources.

[0008] Nucleic acid sequences can be identified according to the method of the invention. One such adeno-associated virus is of the serotype, termed herein serotype 7 (AAV7). Other novel adeno-associated virus serotypes identified by the method include AAV10, AAV11, and AAV12.

[0009] Among particularly desirable AAV fragments which can be identified are the cap proteins, including the vp1, vp2, vp3, the hypervariable regions, the rep proteins, including rep 78, rep 68, rep 52, and rep 40, and the sequences encoding these proteins. Each of these fragments may be readily utilized in a variety of vector systems and host cells. Such fragments may be used alone, in combination with other AAV sequences or fragments, or in combination with elements from other AAV or non-AAV viral sequences. In one particularly desirable embodiment, a vector contains the AAV cap and/or rep sequences.

[0010] As described herein, alignments are performed using any of a variety of publicly or commercially available Multiple Sequence Alignment Programs, such as "Clustal W", accessible through Web Servers on the internet. Alternatively, Vector NTI utilities are also used. There are also a number of algorithms known in the art which can be used to measure nucleotide sequence identity, including those contained in the programs described above. As another example, polynucleotide sequences can be compared using Fasta, a program in GCG Version 6.1. Fasta provides alignments and percent sequence identity of the regions of the best overlap between the query and search sequences. For instance, percent sequence identity between nucleic acid sequences can be determined using Fasta with its default parameters (a word size of 6 and the NOPAM factor for the scoring matrix) as provided in GCG Version 6.1. Similar programs are available for amino acid sequences, e.g., the "Clustal X" program. Generally, any of these programs are used at default settings, although one of skill in the art can alter these settings as needed. Alternatively, one of skill in the art can utilize

another algorithm or computer program which provides at least the level of identity or alignment as that provided by the referenced algorithms and programs.

[0011] The term "substantial homology" or "substantial similarity," when referring to a nucleic acid, or fragment thereof, indicates that, when optimally aligned with appropriate nucleotide insertions or deletions with another nucleic acid (or its complementary strand), there is nucleotide sequence identity in at least about 95 to 99% of the aligned sequences. Preferably, the homology is over full-length sequence, or an open reading frame thereof, or another suitable fragment which is at least 15 nucleotides in length. Examples of suitable fragments are described herein.

[0012] The term "substantial homology" or "substantial similarity," when referring to amino acids or fragments thereof, indicates that, when optimally aligned with appropriate amino acid insertions or deletions with another amino acid, there is amino acid sequence identity in at least about 95 to 99% of the aligned sequences. Preferably, the homology is over full-length sequence, or a protein thereof, e.g., a cap protein, a rep protein, or a fragment thereof which is at least 8 amino acids, or more desirably, at least 15 amino acids in length. Examples of suitable fragments are described herein. [0013] By the term "highly conserved" is meant at least 80% identity, preferably at least 90% identity, and more preferably, over 97% identity. Identity is readily determined by one of skill in the art by resort to algorithms and computer programs known by those of skill in the art.

[0014] The term "percent sequence identity" or "identical" in the context of nucleic acid sequences refers to the residues in the two sequences which are the same when aligned for maximum correspondence. The length of sequence identity comparison may be over the full-length of the genome, the full-length of a gene coding sequence, or a fragment of at least about 500 to 5000 nucleotides, is desired. However, identity among smaller fragments, e.g. of at least about nine nucleotides, usually at least about 20 to 24 nucleotides, at least about 28 to 32 nucleotides, at least about 36 or more nucleotides, may also be desired. Similarly, "percent sequence identity" may be readily determined for amino acid sequences, over the full-length of a protein, or a fragment thereof. Suitably, a fragment is at least about 8 amino acids in length, and may be up to about 700 amino acids. Examples of suitable fragments are described herein.

[0015] The AAV sequences and fragments thereof are useful in production of rAAV, and are also useful as antisense delivery vectors, gene therapy vectors, or vaccine vectors.

[0016] As described herein, the vectors containing the AAV capsid proteins are particularly well suited for use in applications in which the neutralizing antibodies diminish the effectiveness of other AAV serotype based vectors, as well as other viral vectors. The rAAV vectors are particularly advantageous in rAAV readministration and repeat gene therapy.

[0017] As used throughout this specification and the claims, the terms "comprising" and "including" and their variants are inclusive of other components, elements, integers, steps and the like. Conversely, the term "consisting" and its variants is exclusive of other components, elements, integers, steps and the like.

### I. Methods of the Invention

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# A. Detection of Sequences Via Molecular Cloning

[0018] In one aspect, the invention provides a method of identifying target (unknown) nucleic acid sequences in a sample. This method is particularly well suited for detection of viral sequences which are integrated into the chromosome of a cell, e.g., adeno-associated viruses (AAV) and retroviruses, among others.

[0019] As used herein, a sample is any source containing nucleic acids, e.g., tissue, tissue culture, cells, cell culture, and biological fluids including, without limitation, urine and blood. These nucleic acid sequences may be DNA or RNA from plasmids, natural DNA or RNA from any source, including bacteria, yeast, viruses, and higher organisms such as plants or animals. DNA or RNA is extracted from the sample by a variety of techniques known to those of skill in the art, such as those described by Sambrook, Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory). The origin of the sample and the method by which the nucleic acids are obtained for application of the method of the invention is not a limitation of the present invention. Optionally, the method of the invention can be performed directly on the source of DNA, or on nucleic acids obtained (e.g., extracted) from a source.

[0020] The method of the invention involves subjecting a sample containing DNA to amplification via polymerase chain reaction (PCR) using a first set of primers specific for a first region of double-stranded nucleic acid sequences, thereby obtaining amplified sequences.

[0021] As used herein, each of the "regions" is predetermined based upon the alignment of the nucleic acid sequences of at least two serotypes (e.g., AAV) or strains (e.g., lentiviruses), and wherein each of said regions is composed of sequences having a 5' end which is highly conserved, a middle which is variable, and a 3' end which is highly conserved, each of these being conserved or variable relative to the sequences of at least AAV1-AAV6. The 5' and 3' ends are highly conserved over at least 18 base pairs (bp). However, one or both of the sequences at the 5' or 3' end may be conserved over more than 18 bp, more than 25 bp, more than 30 bp, or more than 50 bp at the 5' end. With respect to the variable region, there is no requirement for conserved sequences, these sequences may be relatively conserved, or may have less than 90, 80, or 70% identity among the aligned serotypes or strains.

[0022] Each of the regions may span about 100 bp to about 10 kilobase pairs in length, provided that the first region is at least 250 bp in length. However, it is particularly desirable that one of the regions is a "signature region", i.e., a region which is sufficiently unique to positively identify the amplified sequence as being from the target source. For example, in one embodiment, the first region is about 250 bp in length, and is sufficiently unique among known AAV sequences, that it positively identifies the amplified region as being of AAV origin. Further, the variable sequences within this region are sufficiently unique that can be used to identify the serotype from which the amplified sequences originate. Once amplified (and thereby detected), the sequences can be identified by performing conventional restriction digestion and comparison to restriction digestion patterns for this region in any of AAV1, AAV2, AAV3, AAV4, AAV5, or AAV6, or that of AAV7, AAV10, AAV11, AAV12, or any of the other novel serotypes identified by the invention, which is predetermined and provided by the present invention.

[0023] Given the guidance provided herein, one of skill in the art can readily identify such regions among other integrated viruses to permit ready detection and identification of these sequences. Thereafter, an optimal set of generic primers located within the highly conserved ends can be designed and tested for efficient amplification of the selected region from samples. This aspect of the invention is readily adapted to a diagnostic kit for detecting the presence of the target sequence (e.g., AAV) and for identifying the AAV serotype, using standards which include the restriction patterns for the AAV serotypes described herein or isolated using the techniques described herein. For example, quick identification or molecular serotyping of PCR products can be accomplished by digesting the PCR products and comparing restriction patterns.

[0024] Thus, in one embodiment, the "signature region" for AAV spans about bp 2800 to about 3200 of AAV 1 [SEQ ID NO:6], and corresponding base pairs in AAV 2, AAV3, AAV4, AAV5, and AAV6. More desirably, the region is about 250 bp, located within bp 2886 to about 3143 bp of AAV 1 [SEQ ID NO:6], and corresponding base pairs in AAV 2 [SEQ ID NO:7], AAV3 [SEQ ID NO8], and other AAV serotypes. To permit rapid detection of AAV in the sample, primers which specifically amplify this signature region are utilized. However, the present invention is not limited to the exact sequences identified herein for the AAV signature region, as one of skill in the art may readily alter this region to encompass a shorter fragment, or a larger fragment of this signature region.

[0025] The PCR primers are generated using techniques known to those of skill in the art. Each of the PCR primer sets is composed of a 5' primer and a 3' primer. See, e.g., Sambrook et al, cited herein. The term "primer" refers to an oligonucleotide which acts as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product which is complementary to a nucleic acid strand is induced. The primer is preferably single stranded. However, if a double stranded primer is utilized, it is treated to separate its strands before being used to prepare extension products. The primers may be about 15 to 25 or more nucleotides, and preferably at least 18 nucleotides. However, for certain applications shorter nucleotides, e.g., 7 to 15 nucleotides are utilized.

[0026] The primers are selected to be sufficiently complementary to the different strands of each specific sequence to be amplified to hybridize with their respective strands. Therefore, the primer sequence need not reflect the exact sequence of the region being amplified. For example, a non-complementary nucleotide fragment may be attached to the 5' end of the primer, with the remainder of the primer sequence being completely complementary to the strand. Alternatively, non-complementary bases or longer sequences can be interspersed into the primer, provided that the primer sequence has sufficient complementarity with the sequence of the strand to be amplified to hybridize therewith and form a template for synthesis of the extension product of the other primer.

[0027] The PCR primers for the signature region are based upon the highly conserved sequences of two or more aligned sequences (e.g., two or more AAV serotypes). The primers can accommodate less than exact identity among the two or more aligned AAV serotypes at the 5' end or in the middle. However, the sequences at the 3' end of the primers correspond to a region of two or more aligned AAV serotypes in which there is exact identity over at least five, preferably, over at least nine base pairs, and more preferably, over at least 18 base pairs at the 3' end of the primers. Thus, the 3' end of the primers is composed of sequences with 100% identity to the aligned sequences over at least five nucleotides. However, one can optionally utilize one, two, or more degenerate nucleotides at the 3' end of the primer. [0028] For example, the primer set for the signature region of AAV was designed based upon a unique region within the AAV capsid, as follows. The 5' primer was based upon nt 2867-2891 of AAV2 [SEQ ID NO:7], 5'-GGTAATTCCTCCGGAAATTGGCATT3'. The 3' primer was designed based upon nt 3096-3122 of AAV2 [SEQ ID NO:7], 5'-GACTCATCAACAACAACTGGGGATTC-'3. However, one of skill in the art may have readily designed the primer set based upon the corresponding regions of AAV 1, AAV3, AAV4, AAV5, AAV6, or based upon the information provided herein, AAV7. AAV10, AAV11, AAV12, or another novel AAV. In addition, still other primer sets can be readily designed to amplify this signature region, using techniques known to those of skill in the art.

## B. Isolation of Target Sequences

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[0029] As described herein, the present invention uses a first primer set which specifically amplifies the signature region of the target sequence, e.g., an AAV serotype, in order to permit detection of the target. In a situation in which

further sequences are desired, e.g., if a novel AA V serotype is identified, the signature region may be extended. Thus, the invention may further utilize one or more additional primer sets.

[0030] Suitably, these primer sets are designed to include either the 5' or 3' primer of the first primer set and a second primer unique to the primer set, such that the primer set amplifies a region 5' or 3' to the signature region which anneals to either the 5' end or the 3' end of the signature region. For example, a first primer set is composed of a 5' primer, P1 and a 3' primer P2 to amplify the signature region. In order to extend the signature region on its 3' end, a second primer set is composed of primer P1 and a 3' primer P4, which amplifies the signature region and contiguous sequences downstream of the signature region. In order to extend the signature region on its 5' end, a third primer set is composed of a 5' primer, P5, and primer P2, such that the signature region and contiguous sequences upstream of the signature region are amplified. These extension steps are repeated (or performed at the same time), as needed or desired. Thereafter, the products results from these amplification steps are fused using conventional steps to produce an isolated sequence of the desired length.

[0031] The second and third primer sets are designed, as with the primer set for the signature region, to amplify a region having highly conserved sequences among the aligned sequences. Reference herein to the term "second" or "third" primer set is for each of discussion only, and without regard to the order in which these primers are added to the reaction mixture, or used for amplification. The region amplified by the second primer set is selected so that upon amplification it anneals at its 5' end to the 3' end of the signature region. Similarly, the region amplified by the third primer set is selected so that upon amplification it anneals at its 3' end anneals to the 5' end of the signature region. Additional primer sets can be designed such that the regions which they amplify anneal to the either the 5' end or the 3' end of the extension products formed by the second or third primer sets, or by subsequent primer sets.

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[0032] For example, where AAV is the target sequence, a first set of primers (P1 and P2) are used to amplify the signature region from the sample. In one desirable embodiment, this signature region is located within the AAV capsid. A second set of primers (P1 and P4) is used to extend the 3' end of the signature region to a location in the AAV sequence which is just before the AAV 3' ITR, i.e., providing an extension product containing the entire 3' end of the AAV capsid when using the signature region as an anchor. In one embodiment, the P4 primer corresponds to nt 4435 to 4462 of AAV2 [SEQ ID NO:7], and corresponding sequences in the other AAV serotypes. This results in amplification of a region of about 1.6 kb, which contains the 0.25 kb signature region. A third set of primers (P3 and P2) is used to extend the 5' end of signature region to a location in the AAV sequences which is in the 3' end of the rep genes, i.e., providing an extension product containing the entire 5' end of the AAV capsid when using the signature region as an anchor. In one embodiment, the P3 primer corresponds to nt 1384 to 1409 of AAV2 [SEQ ID NO:7], and corresponding sequences in the other AAV serotypes. This results in amplification of a region of about 1.7 kb, which contains the 0.25 kb signature region. Optionally, a fourth set of primers are used to further extend the extension product containing the entire 5' end of the AAV capsid to also include the rep sequences. In one embodiment, the primer designated P5 corresponds to nt 108 to 133 of AAV2 [SEQ ID NO:7], and corresponding sequences in the other AAV serotypes and is used in conjunction with the P2 primer.

[0033] Following completion of the desired number of extension steps, the various extension products are fused, making use of the signature region as an anchor or marker, to construct an intact sequence. In the example provided herein, AAV sequences containing, at a minimum, an intact AAV cap gene are obtained. Larger sequences may be obtained, depending upon the number of extension steps performed.

[0034] Suitably, the extension products are assembled into an intact AAV sequence using methods known to those of skill in the art. For example, the extension products may be digested with Dralll, which cleaves at the Dralll site located within the signature region, to provide restriction fragments which are re-ligated to provide products containing (at a minimum) an intact AAV cap gene. However, other suitable techniques for assembling the extension products into an intact sequence may be utilized. See, generally, Sambrook et al, cited herein.

[0035] As an alternative to the multiple extension steps described above, another embodiment of the invention provides for direct amplification of a 3.1 kb fragment which allows isolation of full-length cap sequences. To directly amplify a 3.1 kb full-length cap fragment from NHP tissue and blood DNAs, two other highly conserved regions were identified in AAV genomes for use in PCR amplification of large fragments. A primer within a conserved region located in the middle of the rep gene is utilized (AV1ns: 5' GCTGCGTCAACTGGACCAATGAGAAC 3', nt of SEQ ID NO:6) in combination with the 3' primer located in another conserved region downstream of the Cap gene (AV2cas: 5' CGCAGAGACCAAAGT-TCAACTGAAACGA 3', SEQ ID NO: 7) for amplification of AAV sequences including the full-length AAV cap. Typically, following amplification, the products are cloned and sequence analysis is performed with an accuracy of ≥ 99.9%. Using this method, the inventors have isolated at least 50 capsid clones which have subsequently been characterized. Among them, 37 clones were derived from Rhesus macaque tissues (rh.1 - rh.37), 6 clones from cynomologous macaques (cy.1 - cy.6), 2 clones from Baboons (bb.1 and bb.2) and 5 clones from Chimps (ch.1 - ch.5). These clones are identified elsewhere in the specification, together with the species of animal from which they were identified and the tissues in that animal these novel sequences have been located.

### II. Diagnostic Kit

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[0036] In another aspect, the invention provides a diagnostic kit as defined in claim 23 hereinafter for detecting the presence of an unknown adeno-associated virus (AAV) in a sample. Such a kit may contain a first set of 5' and 3' PCR primers specific for a signature region of the AAV nucleic acid sequence. Alternatively, or additionally, such a kit can contain a first set of 5' and 3' PCR primers specific for the 3.1 kb fragment which includes the full-length AAV capsid nucleic acid sequence identified herein (e.g., the AV1ns and AV2cas primers.) Optionally, a kit of the invention may further contain two or more additional sets of 5' and 3' primers, as described herein, and/or PCR probes. These primers and probes are used according to the present invention to amplify signature regions of each AAV serotype, e.g., using quantitative PCR.

[0037] Such a kit may further include one or more restriction enzymes, standards for AAV serotypes providing their "signature restriction enzyme digestions analyses", and/or other means for determining the serotype of the AAV detected. [0038] In addition, kits of the invention may include, instructions, a negative and/or positive control, containers, diluents and buffers for the sample, indicator charts for signature comparisons, disposable gloves, decontamination instructions, applicator sticks or containers, and sample preparator cups, as well as any desired reagents, including media, wash reagents and concentration reagents. Such reagents may be readily selected from among the reagents described herein, and from among conventional concentration reagents. In one desirable embodiment, the wash reagent is an isotonic saline solution which has been buffered to physiologic pH, such as phosphate buffered saline (PBS); the elution reagent is PBS containing 0.4 M NaCl, and the concentration reagents and devices. For example, one of skill in the art will recognize that reagents such as polyethylene glycol (PEG), or NH<sub>4</sub>SO<sub>4</sub> may be useful, or that devices such as filter devices. For example, a filter device with a 100 K membrane would concentrate rAAV.

[0039] The kits provided by the present invention are useful for performing the methods described herein, and for study of biodistribution, epidemiology, mode of transmission of novel AAV serotypes in human and NHPs.

[0040] Thus, the methods and kits of the invention permit identification of target AAV sequences, particularly integrated AAV sequences.

[0041] In one notable example, the method of the invention facilitated analysis of cloned AAV sequences by the inventors, which revealed heterogeneity of proviral sequences between cloned fragments from different animals, all of which were distinct from the known six AAV serotypes, with the majority of the variation localized to hypervariable regions of the capsid protein. Surprising divergence of AAV sequences was noted in clones isolated from single tissue sources, such as lymph node, from an individual rhesus monkey. This heterogeneity is best explained by apparent evolution of AAV sequence within ind ividual animals due, in part, to extensive homologous recombination between a limited number of co-infecting parenteral viruses. These studies suggest sequence evolution of widely disseminated virus during the course of a natural AAV infection that presumably leads to the formation of swarms of quasispecies which differ from one another in the array of capsid hypervariable regions. This is the first example of rapid molecular evolution of a DNA virus in a way that formerly was thought to be restricted to RNA viruses.

[0042] Sequences of several novel AAV serotypes identified by the method of the invention and characterization of these serotypes is provided.

III. Novel AAV Serotypes

A. Nucleic Acid Sequences

[0043] Nucleic acid sequences of novel AAV serotypes identified by the methods of the invention are provided. See, SEQ ID NO:1, 9 - 59, and 117 - 120. See also and the sequence listing.

[0044] For novel serotype AAV7, the full-length sequences, including the AAV 5' ITRs, capsid, rep, and AAV 3' ITRs are provided in SEQ ID NO:1.

[0045] For other novel AA V serotypes, the approximately 3.1 kb fragment isolated according to the method of the invention is provided. This fragment contains sequences encoding full-length capsid protein and all or part of the sequences encoding the rep protein. These sequences include the clones identified below.

[0046] For still other novel AAV serotypes, the signature region encoding the capsid protein is provided. For example, the AAV10 nucleic acid sequences include those illustrated in See, SEQ ID NO:117, which spans 255 bases. The AAV11 nucleic acid sequences include the DNA sequences illustrated in SEQ ID NO:118 which spans 258 bases. The AAV12 nucleic acid sequences include the DNA sequences illustrated in SEQ ID NO: 119, which consists of 255 bases. Using the methodology described above, further AAV10, AAV11 and AAV 12 sequences can be readily identified and used for a variety of purposes, including those described for AAV7 and the other novel serotypes herein.

[0047] Novel NHP sequences identified by the invention include those provided in the following Table I, which are identified by clone number:

# Table 1

AAV Cap Sequence	Clone Number	Source		
	·	Species	Tissue	SEQ ID NO (DNA)
[Rh.I]	Clone 9 <sup>-</sup> (AAV9)	Rhesus	Heart	5
Rh.2	Clone 43.1	Rhesus	MLN	. 39
Rh.3	Clone 43.5	Rhesus	MLN	40
Rh.4	Clone 43.12	Rhesus	MLN	41
Rh.5	Clone 43.20	Rhesus	MLN	42
Rh.6	Clone 43.21	Rhesus	MLN	43
Rh.7	Clone 43.23	Rhesus	MLN	44

# Table 1 (cont'd)

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Rh.8	Clone 43.25		MLN	45
Rh.9	Clone 44.1	Rhesus	Liver	46
Rh.10	Clone 44.2	Rhesus	Liver	59
Rh.11	Clone 44.5	Rhesus	Liver	47
Rh.12	Clone	Rhesus	MLN	30
	42.1B			
Rh.13	42.2	Rhesus	MLN	9
Rh.14	Clone	Rhesus	MLN	32
	42.3A			
Rh.15	Clone	Rhesus	MLN	36
	42.3B			
Rh.16	Clone 42.4	Rhesus	MLN	33
Rh.17	Clone	Rhesus	MLN	34
	42.5A			
Rh.18	Clone	Rhesus	MLN	29
	42.5B			
Rh.19	Clone	Rhesus	MLN	38
	42.6B			
Rh.20	Clone 42.8	Rhesus	MLN	27
Rh.21	Clone 42.10	Rhesus	MLN	35
Rh.22	Clone 42.11	Rhesus	MLN	37
Rh.23	Clone 42.12	Rhesus	MLN	58
Rh.24	Clone 42.13	Rhesus	MLN	31
Rh.25	Clone 42.15	Rhesus	MLN	28
Rh.26_	Clone 223.2	Rhesus	Liver	49
Rh.27	Clone 223.4	Rhesus	Liver	50
Rh.28	Clone 223.5	Rhesus	Liver	51
Rh.29	Clone 223.6	Rhesus	Liver	52
Rh.30	Clone 223.7	Rhesus	Liver	53
Rh.31	Clone	Rhesus	Liver	48
	223.10		<del></del>	
Rh.32	Clone C1	Rhesus	Spleen, Duo,	19
			Kid & Liver	
Rh.33	Clone C3	Rhesus		20
Rh.34	Clone C5	Rhesus		21
Rh.35	Clone F1	Rhesus	Liver	22
Rh.36	Clone F3	Rhesus		23
Rh.37	Clone F5	Rhesus		24
Cy.1	Clone 1.3	Cyno	Blood	14
Cy.2	Clone	Cyno	Blood	15
	13.3B			
Cy.3	Clone 24.1	Cyno	Blood	16
Cy.4	Clone 27.3	Cyno	Blood	17
Cy.5 Cy.6	Clone 7.2	Супо	Blood	18
	Clone 16.3			

	Table 1 (cont'd)									
bb.l	Clone 29.3	Baboon	Blood	11						
bb.2	Clone 29.5	Baboon	Blood	13						
Ch.1	Clone A3.3	Chimp	Blood	57						
Ch.2	Clone A3.4	Chimp	Blood	54						
Ch.3	Clone A3.5	Chimp	Blood	55						
Ch.4	Cione A3.7	Chimp	Blood,	56						

[0048] A novel NHP clone was made by splicing capsids fragments of two chimp adenoviruses into an AAV2 rep construct. This new clone, A3.1, is also termed Ch.5 [SEQ ID NO:20]. Additionally, the present invention includes two human AAV sequences, termed H6 [SEQ ID NO:25] and H2 [SEQ ID NO:26].

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[0049] The AAV nucleic acid sequences further encompass the strand which is complementary to the strands provided in the sequences provided in the Sequence Listing [SEQ ID NO:1, 9 - 59, 117-120], nucleic acid sequences, as well as the RNA and cDNA sequences corresponding to the sequences provided in the Sequence Listing [SEQ ID NO:1, 9 - 59, 117-120], and their complementary strands. Also included in the nucleic acid sequences are natural variants and engineered modifications of the sequences of the Sequence Listing [SEQ ID NO:1, 9 - 59, 117-120], and their complementary strands. Such modifications include, for example, labels which are known in the art, methylation, and substitution of one or more of the naturally occurring nucleotides with a degenerate nucleotide.

[0050] Further included are nucleic acid sequences which are greater than 85%, preferably at least about 90%, more preferably at least about 95%, and most preferably at least about 98 to 99% identical or homologous to the sequences of the invention, including the Sequence Listing [SEQ ID NO:1, 9 - 59, 117-120]. These terms are as defined herein.

[0051] Also included are fragments of the novel AAV sequences identified by the method described herein. Suitable fragments are at least 15 nucleotides in length, and encompass functional fragments, i.e., fragments which are of biological interest. In one embodiment, these fragments are fragments of the novel sequences of the Sequence Listing [SEQ ID NO:1, 9 - 59, 117-120], their complementary strands, cDNA and RNA complementary thereto.

[0052] Examples of suitable fragments are provided with respect to the location of these fragments on AAV1, AAV2, or AAV7. However, using the alignment provided herein (obtained using the Clustal W program at default settings), or similar techniques for generating an alignment with other novel serotypes of the invention, one of skill in the art can readily identify the precise nucleotide start and stop codons for desired fragments.

[0053] Examples of suitable fragments include the sequences encoding the three variable proteins (vp) of the AAV capsid which are alternative splice variants: vp1 [e.g., nt 825 to 3049 of AA V7, SEQ ID NO: 1]; vp2 [e.g., nt 1234 - 3049 of AAV7, SEQ ID NO: 1]; and vp 3 [e.g., nt 1434 - 3049 of AAV7, SEQ ID NO:1]. It is notable that AAV7 has an unusual GTG start codon. With the exception of a few house-keeping genes, such a start codon has not previously been reported in DNA viruses. The start codons for vp1, vp2 and vp3 for other AAV serotypes have been believed to be such that they permit the cellular mechanism of the host cell in which they reside to produce vp1, vp2 and vp3 in a ratio of 10%:10%:80%, respectively, in order to permit efficient assembly of the virion. However, the AAV7 virion has been found to assemble efficiently even with this rare GTG start codon. Thus, the inventors anticipate this it is desirable to alter the start codon of the vp3 of other AAV serotypes to contain this rare GTG start codon, in order to improve packaging efficiency, to alter the virion structure and/or to alter location of epitopes (e.g., neutralizing antibody epitopes) of other AAV serotypes. The start codons may be altered using conventional techniques including, e.g., site directed mutagenesis. The altered AAV virions may be of any selected serotype, composed of a vp 3, and/or optionally, vp 1 and/or vp2 having start codons altered to GTG.

[0054] Other suitable fragments of AAV, include a fragment containing the start codon for the AAV capsid protein [e.g., nt 468 to 3090 of AAV7, SEQ ID NO:1, nt 725 to 3090 of AAV7, SEQ ID NO:1, and corresponding regions of the other AAV serotypes]. Still other fragments of AAV7 and the other novel AAV semtypes identified using the methods described herein include those encoding the rep proteins, including *rep* 78 [e.g., initiation codon 334 for AAV7], *rep* 68 [initiation codon nt 334 for AAV7], *rep* 52 [initiation codon 1006 for AAV7], and *rep* 40 [initiation codon 1006 for AAV7] Other fragments of interest may include the AAV 5' inverted terminal repeats ITRs, [nt 1 to 107 for AAV7]; the AA V 3' ITRs [nt 4704 to 4721 for AAV7], P19 sequences. AAV P40 sequences, the rep binding site, and the terminal resolute site (TRS). Still other suitable fragments wilt be readily apparent to those of skill in the art.

[0055] In addition to the nucleic acid sequences provided in the figures and Sequence Listing, there are nucleic acid molecules and sequences which are designed to express the amino acid sequences, proteins and peptides of the AAV serotypes of the invention. These include nucleic acid sequences which encode the following novel AAV amino acid sequences: C1 [SEQ ID NO:60], C2 [SEQ ID NO:61], C5 [SEQ ID NO:62], A3-3 [SEQ ID NO:66], A3-7 [SEQ ID NO:67],

A3-4 [SEQ ID NO:68], A3-5 [SEQ ID NO: 69], 3.3b [SEQ ID NO: 62], 223.4 [SEQ ID NO: 73], 223-5 [SEQ ID NO:74], 223-10 [SEQ ID NO:75], 223-2 [SEQ ID NO:76], 223-7 [SEQ ID NO: 77], 223-6 [SEQ ID NO: 78], 44-1 [SEQ ID NO: 79], 44-5 [SEQ ID NO:80], 44-2 [SEQ ID NO:81], 42-15 [SEQ ID NO: 84], 42-8 [SEQ ID NO: 85], 42-13 [SEQ ID NO:86], 42-3A [SEQ ID NO:87], 42-4 [SEQ ID NO:88], 42-5A [SEQ ID NO:89], 42-1B [SEQ ID NO:90], 42-5B [SEQ ID NO:91], 43-1 [SEQ ID NO: 92], 43-12 [SEQ ID NO: 93], 43-5 [SEQ ID NO:94], 43-21 [SEQ ID NO:96], 43-25 [SEQ ID NO: 97], 43-20 [SEQ ID NO:99], 24.1 [SEQ ID NO: 101], 42.2 [SEQ ID NO:102], 7.2 [SEQ ID NO: 103], 27.3 [SEQ ID NO: 104], 16.3 [SEQ ID NO: 105], 42.10 [SEQ ID NO: 106], 42-38 [SEQ ID NO: 107], 42-11 [SEQ ID NO: 108], F1 [SEQ ID NO: 109], F5 [SEQ ID NO: 110], F3 [SEQ ID NO:111], 42-6B [SEQ ID NO: 112], and/or 42-12 [SEQ ID NO: 113], and artificial AAV serotypes generated using these sequences and/or unique fragments thereof.

[0056] As used herein, artificial AAV serotypes include, without limitation. AAV with a non-naturally occurring capsid protein. Such an artificial capsid may be generated by any suitable technique, using a novel AAV sequence (e.g., a fragment of a vp1 capsid protein) in combination with heterologous sequences which may be obtained from another AAV serotype (known or novel), non-contiguous portions of the same AAV serotype, from a non-AAV viral source, or from a non-viral source. An artificial AAV serotype may be, without limitation, a chimeric AAV capsid, a recombinant AAV capsid, or a "humanized" AAV capsid.

### B. AAV Amino Acid Sequences, Proteins and Peptides

[0057] The invention provides proteins and fragments thereof which are encoded by the nucleic acid sequences of the novel AAV serotypes identified herein, including, e.g., AA V7 [nt 825 to 3049 of AA V7, SEQ ID NO: 1] the other novel serotypes provided herein. Thus, the capsid proteins of the novel serotypes of the invention, including: H6 [SEQ ID NO: 25], H2 [SEQ ID NO: 26], 42-2 [SEQ ID NO:9], 42-8 [SEQ ID NO:27], 42-15 [SEQ ID NO:28], 42-5b [SEQ ID NO: 29], 42-1b [SEQ ID NO:30]; 42-13 [SEQ ID NO: 31], 42-3a [SEQ ID NO: 32], 42-4 [SEQ ID NO:33], 42-5a [SEQ ID NO: 34], 42-10 [SEQ ID NO:35], 42-3b [SEQ ID NO: 36], 42-11 [SEQ ID NO: 37], 42-6b [SEQ ID NO:38], 43-1 [SEQ ID NO: 39], 43-5 [SEQ ID NO: 40], 43-12 [SEQ ID NO:41], 43-20 [SEQ ID NO:42], 43-21 [SEQ ID NO: 43], 43-23 [SEQ ID NO:44], 43-25 [SEQ ID NO: 45], 44.1 [SEQ ID NO:47], 44.5 [SEQ ID NO:47], 223.10 [SEQ ID NO:48], 223.2 [SEQ ID NO:49], 223.4 [SEQ ID NO:50], 223.5 [SEQ ID NO:51], 223.6 [SEQ ID NO:57], 42.12 [SEQ ID NO: 58], and 44.2 [SEQ ID NO: 59], can be readily generated using conventional techniques from the open reading frames provided for the above-listed clones.

[0058] The sequences, proteins, and fragments may be produced by any suitable means, including recombinant production, chemical synthesis, or other synthetic means. Such production methods are within the knowledge of those of skill in the art.

### 35 IV. Production of rAAV with novel AAV capsids

[0059] Novel, wild-type AAV serotypes can be identified by the invention, the sequences of which wild-type AAV serotypes are free of DNA and/or cellular material with these viruses are associated in nature. In another aspect, the present invention provides molecules which utilize the novel AAV sequences of the invention, including fragments thereof, for production of molecules useful in delivery of a heterologous gene or other nucleic acid sequences to a target cell.

[0060] The following examples illustrate several aspects and embodiments of the invention.

### **EXAMPLES**

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Example 1: PCR amplification, cloning and characterization of novel AAV sequences.

[0061] Tissues from nonhuman primates were screened for AAV sequences using a PCR method based on oligonucleotides to highly conserved regions of known AAVs. A stretch of AAV sequence spanning 2886 to 3143 bp of AAV1 [SEQ ID NO:6] was selected as a PCR amplicon in which a hypervariable region of the capsid protein (Cap) that is unique to each known AAV serotype, which is termed herein a "signature region," is flanked by conserved sequences. In later analysis, this signature region was shown to be located between conserved residues spanning hypervariable region 3.

[0062] An initial survey of peripheral blood of a number of nonhuman primate species revealed detectable AAV in a subset of animals from species such as rhesus macaques, cynomologous macaques, chimpanzees and baboons. However, there were no AAV sequences detected in some other species tested, including Japanese macaques, pig-tailed macaques and squirrel monkeys. A more extensive analysis of vector distribution was conducted in tissues of rhesus monkeys of the University of Pennsylvania and Tulane colonies recovered at necropsy. This revealed AAV sequence throughout a wide array of tissues.

## A. Amplification of an AAV signature region

[0063] DNA sequences of AAV1-6 and AAVs isolated from Goose and Duck were aligned to each other using "Clustal W" at default settings. Sequence similarities among AAVs were compared.

[0064] In the line of study, a 257 bp region spanning 2886 bp to 3143 bp of AAV 1 [SEQ ID NO: 6], and the corresponding region in the genomes of AAV 2-6 genomes was identified by the inventors. This region is located with the AAV capsid gene and has highly conserved sequences among at both 5' and 3' ends and is relatively variable sequence in the middle. In addition, this region contains a DrallI restriction enzyme site (CACCACGTC, SEQ ID NO:15). The inventors have found that this region serves as specific signature for each known type of AAV DNA. In other words, following PCR reactions, digestion with endonucleases that are specific to each known serotypes and gel electrophoresis analysis, this regions can be used to definitively identify amplified DNA as being from serotype 1, 2, 3, 4, 5, 6, or another serotype.

[0065] The primers were designed, validated and PCR conditions optimized with AAV1, 2 and 5 DNA controls. The primers were based upon the sequences of AAV2: 5' primer, 15: bp 2867-2891 of AAV2 (SEQ ID NO:7) and 3' primer,

18as, bp 3095-3121 of AAV2 (SEQ ID NO:7).

[0066] Cellular DNAs from different tissues including blood, brain, liver, lung, testis, etc. of different rhesus monkeys were studied utilizing the strategy described above. The results revealed that DNAs from different tissues of these monkeys gave rise to strong PCR amplifications. Further restriction analyses of PCR products indicated that they were

amplified from AAV sequences different from any published AAV sequences.

[0067] PCR products (about 255 bp in size) from DNAs of a variety of monkey tissues have been cloned and sequenced. Bioinformatics study of these novel AAV sequences indicated that they are novel AAV sequences of capsid gene and distinct from each other. Multiple sequence alignment analysis was performed using the Clustal W (1.81) program. The percentage of sequence identity between the signature regions of AAV 1-7 and AAV 10-12 genomes is provided below.

Table 1. Sequences for Analysis

Table 1. Sequences for Analysis								
Sequence#	AAV Serotype	Size (bp)						
1	AAV1	258						
2 .	AAV2	255						
3	AAV3	255						
4	AAV4	246						
5	AAV5	258						
6	AAV6	258						
7	AAV7	258						
10	AAV10	255						
11	AAV11	258						
12	AAV12	255						

Table 3. Pairwise Alignment (Percentage of Identity)

	AAV2	AAV3	AAV4	AAV5	AAV6	AAV7	AAV10	AAV11	AAV12
AAV1	90	90	81	76	97	91	93	94	93
AAV2		93	79	78	90	90	93	93	92
AAV3			80	76	90	92	92	92	92
AAV4				76	81	84	82	81	79
AAV5					75	78	79	79	76
AAV6						91	92	94	94
AAV7							94	92	92
AAV10								95	93

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#### Table continued

	AAV2	AAV3	AAV4	AAV5	AAV6	AAV7	AAV10	AAV11	AAV12
AAV11									94

[0068] Over 300 clones containing novel AAV serotype sequences that span the selected 257 bp region were isolated and sequenced. Bioinformatics analysis of these 300+ clones suggests that this 257 bp region is critical in serving as a good land marker or signature sequence for quick isolation and identification of novel AAV serotype.

B. Use of the signature region for PCR amplification.

[0069] The 257 bp signature region was used as a PCR anchor to extend PCR amplifications to 5' of the genome to cover the junction region of rep and cap genes (1398 bp - 3143 bp, SEQ ID NO:6) and 3' of the genome to obtain the entire cap gene sequence (2866 bp - 4600 bp, SEQ ID NO:6). PCR amplifications were carried out using the standard conditions, including denaturing at 95°C for 0.5-1 min, annealing at 60-65°C for 0.5-1 min and extension at 72° C for I min per kb with a total number of amplification cycles ranging from 28 to 42.

[0070] Using the aligned sequences as described in "A", two other relative conserved regions were identified in the sequence located in 3' end of rep genes and 5' to the 257 bp region and in the sequence down stream of the 257 bp fragment but before the AAV' 3 ITR. Two sets of new primers were designed and PCR conditions optimized for recovery of entire capsid and a part of rep sequences of novel AAV serotypes. More specifically, for the 5' amplification, the 5' primer, AV1Ns, was GCTGCGTCAACTGGACCAATGAGAAC [nt 1398-1423 of AAV1, SEQ ID NO:6] and the 3' primer was 18as, identified above. For the 3' amplification, the 5' primer was 1s, identified above, and the 3' primer was AV2Las, TCGTTTCAGTTGAACTTTGGTCTCTGCG [nt 4435-4462 of AAV2, SEQ ID NO:7].

[0071] In these PCR amplifications, the 257 bp region was used as a PCR anchor and land marker to generate overlapping fragments to construct a complete capsid gene by fusion at the DrallI site in the signature region following amplification of the 5' and 3' extension fragments obtained as described herein. More particularly, to generate the intact AAV7 cap gene, the three amplification products (a) the sequences of the signature region; (b) the sequences of the 5' extension; and (c) the sequences of the 3' extension were cloned into a pCR4-Topo [Invitrogen] plasmid backbone according to manufacturer's instructions. Thereafter, the plasmids were digested with DrallI and recombined to form an intact cap gene.

[0072] In this line of work, about 80 % of capsid sequences of AAV7 and AAV 8 were isolated and analyzed. Another novel serotype, AAV9, was also discovered from Monkey #2.

[0073] Using the PCR conditions described above, the remaining portion of the rep gene sequence for AAV7 is isolated and cloned using the primers that amplify 108 bp to 1461 bp of AAV genome (calculated based on the numbering of AAV2, SEQ ID NO:7). This clone is sequenced for construction of a complete AAV7 genome without ITRs.

### C. Direct Amplification of 3.1 kb Cap fragment

[0074] To directly amplify a 3.1 kb full-length Cap fragment from NHP tissue and blood DNAs, two other highly conserved regions were identified in AAV genomes for use in PCR amplification of large fragments. A primer within a conserved region located in the middle of the rep gene was selected (AV1ns: 5' GCTGCGTCAACTGGACCAATGAGAAC 3', nt 1398-1423 of SEQ ID NO:6) in combination with the 3' primer located in another conserved region downstream of the Cap gene (AV2cas: 5' CGCAGAGACCAAAGTTCAACTGAAACGA 3', SEQ ID NO:7) for amplification of full-length cap fragments. The PCR products were Topo-cloned according to manufacturer's directions (Invitrogen) and sequence analysis was performed by Qiagengenomics (Qiagengenomics, Seattle, WA) with an accuracy of ≥ 99.9%. A total of 50 capsid clones were isolated and characterized. Among them, 37 clones were derived from Rhesus macaque tissues (rh.1 - rh.37), 6 clones from cynomologous macaques (cy.1 - cy.6), 2 clones from Baboons (bb.1 and bb.2) and 5 clones from Chimps (ch.1 - ch.5).

[0075] To rule out the possibility that sequence diversity within the novel AAV family was not an artifact of the PCR, such as PCR-mediated gene splicing by overlap extension between different partial DNA templates with homologous sequences, or the result of recombination process in bacteria, a series of experiments were performed under identical conditions for VP1 amplification-using total cellular DNAs. First, intact AAV7 and AAV8 plasmids were mixed at an equal molar ratio followed by serial dilutions. The serially diluted mixtures were used as templates for PCR amplification of 3.1 kb VP1 fragments using universal primers and identical PCR conditions to that were used for DNA amplifications to see whether any hybrid PCR products were generated. The mixture was transformed into bacteria and isolated transformants to look for hybrid clones possibly derived from recombination process in bacterial cells. In a different experiment, we restricted AAV7 and AAV8 plasmids with Msp I, Ava I and Hael, all of which cut both genomes multiple times at different

positions, mixed the digestions in different combinations and used them for PCR amplification of VP1 fragments under the same conditions to test whether any PCR products could be generated through overlap sequence extension of partial AAV sequences. In another experiment, a mixture of gel purified 5' 1.5 kb AAV7 VP1 fragment and 3' 1.7 kb AAV8 VP1 fragment with overlap in the signature region was serially diluted and used for PCR amplification in the presence and absence of 200 ng cellular DNA extracted from a monkey cell line that was free of AAV sequences by TaqMan analysis. None of these experiments demonstrated efficient PCR-mediated overlap sequence production under the conditions of the genomic DNA Cap amplification (data not shown). As a further confirmation, 3 pairs of primers were designed, which were located at different HVRs, and were sequence specific to the variants of clone 42s from Rhesus macaque F953, in different combinations to amplify shorter fragments from mesenteric lymph node (MLN) DNA from F953 from which clone 42s were isolated. All sequence variations identified in full-length Cap clones were found in these short fragments (data not shown).

Example 2: Adeno-Associated Viruses Undergo Substantial Evolution in Primates During Natural Infections

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[0076] Sequence analysis of selected AAV isolates revealed divergence throughout the genome that is most concentrated in hypervariable regions of the capsid proteins. Epidemiologic data indicate that all known serotypes are endemic to primates, although isolation of clinical isolates has been restricted to AAV2 and AAV3 from anal and throat swabs of human infants and AAV5 from a human condylomatous wart. No known clinical sequalae have been associated with AAV infection.

[0077] In an attempt to better understand the biology of AAV, nonhuman primates were used as models to characterize the sequiae of natural infections. Tissues from nonhuman primates were screened for AAV sequences using the PCR method of the invention based on oligonucleotides to highly conserved regions of known AAVs (see Example 1). A stretch of AAV sequence spanning 2886 to 3143 bp of AAV1 [SEQ ID NO:6] was selected as a PCR amplicon in which conserved sequences are flanked by a hypervariable region that is unique to each known AAV serotype, termed herein a "signature region."

[0078] An initial survey of peripheral blood of a number of nonhuman primate species including rhesus monkeys, cynomologous monkeys, chimpanzees, and baboons revealed detectable AAV in a subset of animals from all species. A more extensive analysis of vector distribution was conducted in tissues of rhesus monkeys of the University of Pennsylvania and Tulane colonies recovered at necropsy. This revealed AAV sequence throughout a wide array of tissues. [0079] The amplified signature sequences were subcloned into plasmids and individual transformants were subjected to sequence analysis. This revealed substantial variation in nucleotide sequence of clones derived from different animals. Variation in the signature sequence was also noted in clones obtained within individual animals. Tissues harvested from two animals in which unique signature sequences were identified (i.e., colon from 98E044 and heart from 98E056) were further characterized by expanding the sequence amplified by PCR using oligonucleotides to highly conserved sequences. In this way, complete proviral structures were reconstructed for viral genomes from both tissues as described herein. These proviruses differ from the other known AAVs with the greatest sequence divergence noted in regions of the Cap gene.

[0080] Additional experiments were performed to confirm that AAV sequences resident to the nonhuman primate tissue represented proviral genomes of infectious virus that is capable of being rescued and form virions. Genomic DNA from liver tissue of animal 98E056, from which AAV8 signature sequence was detected, was digested with an endonuclease that does not have a site within the AAV sequence and transfected into 293 cells with a plasmid containing an E1 deleted genome of human adenovirus serotype 5 as a source of helper functions. The resulting lysate was passaged on 293 cells once and the lysate was recovered and analyzed for the presence of AAV Cap proteins using a broadly reacting polyclonal antibody to Cap proteins and for the presence and abundance of DNA sequences from the PCR amplified AAV provirus from which AAV8 was derived. Transfection of endonuclease restricted heart DNA and the adenovirus helper plasmid yielded high quantities of AAV8 virus as demonstrated by the detection of Cap proteins by Western blot analysis and the presence of 10<sup>4</sup> AAV8 vector genomes per 293 cell. Lysates were generated from a large-scale preparation and the AAV was purified by cesium sedimentation. The purified preparation demonstrated 26 nm icosohedral structures that look identical to those of AAV serotype 2. Transfection with the adenovirus helper alone did not yield AAV proteins or genomes, ruling out contamination as a source of the rescued AAV.

[0081] To further characterize the inter and intra animal variation of AAV signature sequence, selected tissues were subjected to extended PCR to amplify entire Cap open reading frames.

[0082] The resulting fragments were cloned into bacterial plasmids and individual transformants were isolated and fully sequenced. This analysis involved mesenteric lymph nodes from three rhesus monkeys (Tulane/V223 - 6 clones; Tulane/T612 - 7 clones; Tulane/F953 - 14 clones), liver from two rhesus monkeys (Tulane/V251 - 3 clones; Penn/00E033 - 3 clones), spleen from one rhesus monkey (Penn/97E043 - 3 clones), heart from one rhesus monkey (IHGT/98E046-1 clone) and peripheral blood from one chimpanzee (New Iberia/X133 - 5 clones), six cynomologous macaques (Charles River/A1378, A3099, A3388, A3442, A2821, A3242 - 6 clones total) and one Baboon (SFRB/8644 - 2 clones). Of the

50 clones that were sequenced from 15 different animals, 30 were considered non-redundant based on the finding of at least 7 amino acid differences from one another. The non-redundant VP1 clones are numbered sequentially as they were isolated, with a prefix indicating the species of non-human primate from which they were derived. The structural relationships between these 30 non-redundant clones and the previously described 8 AAV serotypes were determined using the SplitsTree program [Huson, D. H. SplitsTree: analyzing and visualizing evolutionary data. *Bioinformatics* 14, 68-73 (1998)] with implementation of the method of split decomposition. The analysis depicts homoplasy between a set of sequences in a tree-like network rather than a bifurcating tree. The advantage is to enable detection of groupings that are the result of convergence and to exhibit phylogenetic relationships even when they are distorted by parallel events. Extensive phylogenetic research will be required in order to elucidate the AAV evolution, whereas the intention here only is to group the different clones as to their sequence similarity.

[0083] To confirm that the novel VP1 sequences were derived from infectious viral genomes, cellular DNA from tissues with high abundance of viral DNA was restricted with an endonuclease that should not cleave within AAV and transfected into 293 cells, followed by infection with adenovirus. This resulted in rescue and amplification of AAV genomes from DNA of tissues from two different animals (data not shown).

[0084] VP1 sequences of the novel AAVs were further characterized with respect to the nature and location of amino acid sequence variation. All 30 VP1 clones that were shown to differ from one another by greater than 1% amino acid sequence were aligned and scored for variation at each residue. An algorithm developed to determine areas of sequence divergence yielded 12 hypervariable regions (HVR) of which 5 overlap or are part of the 4 previously described variable regions [Kotin, cited above; Rutledge, cited above]. The threefold-proximal peaks contain most of the variability (HVR5-10). Interestingly the loops located at the 2 and 5 fold axis show intense variation as well. The HVRs 1 and 2 occur in the N-terminal portion of the capsid protein that is not resolved in the X-ray structure suggesting that the N-terminus of the VP1 protein is exposed on the surface of the virion.

[0085] Real-time PCR was used to quantify AAV sequences from tissues of 21 rhesus monkeys using primers and probes to highly conserved regions of Rep (one set) and Cap (two sets) of known AAVs. Each data point represents analysis from tissue DNA from an individual animal. This confirmed the wide distribution of AAV sequences, although the quantitative distribution differed between individual animals. The source of animals and previous history or treatments did not appear to influence distribution of AAV sequences in rhesus macaques. The three different sets of primers and probes used to quantify AAV yielded consistent results. The highest levels of AAV were found consistently in mesenteric lymph nodes at an average of 0.01 copies per diploid genome for 13 animals that were positive. Liver and spleen also contained high abundance of virus DNA. There were examples of very high AAV, such as in heart of rhesus macaque 98E056, spleen of rhesus macaque 97E043 and liver of rhesus macaque RQ4407, which demonstrated 1.5, 3 and 20 copies of AAV sequence per diploid genome respectively. Relatively low levels of virus DNA were noted in peripheral blood mononuclear cells, suggesting the data in tissue are not due to resident blood components (data not shown). It should be noted that this method would not necessarily capture all AAVs resident to the nonhuman primates since detection requires high homology to both the oligonucleotides and the real time PCR probe. Tissues from animals with high abundance AAV DNA was further analyzed for the molecular state of the DNA, by DNA hybridization techniques, and its cellular distribution, by *in situ* hybridization.

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[0086] The kind of sequence variation revealed in AAV proviral fragments isolated from different animals and within tissues of the same animals is reminiscent of the evolution that occurs for many RNA viruses during pandemics or even within the infection of an individual. In some situations the notion of a wild-type virus has been replaced by the existence of swarms of quasispecies that evolve as a result of rapid replication and mutations in the presence of selective pressure. One example is infection by HIV, which evolves in response to immunologic and pharmacologic pressure. Several mechanisms contribute to the high rate of mutations in RNA viruses, including low fidelity and lack of proof reading capacity of reverse transcriptase and non-homologous and homologous recombination.

[0087] Evidence for the formation of quasispecies of AAV was illustrated in this study by the systematic sequencing of multiple cloned proviral fragments. In fact, identical sequences could not be found within any extended clones isolated between or within animals. An important mechanism for this evolution of sequence appears to be a high rate of homologous recombination between a more limited number of parenteral viruses. The net result is extensive swapping of hypervariable regions of the Cap protein leading to an array of chimeras that could have different tropisms and serologic specificities (i.e., the ability to escape immunologic responses especially as it relates to neutralizing antibodies). Mechanisms by which homologous recombination could occur are unclear. One possibility is that + and - strands of different single stranded AAV genomes anneal during replication as has been described during high multiplicity of infections with AAV recombinants. It is unclear if other mechanisms contribute to sequence evolution in AAV infections. The overall rate of mutation that occurs during AAV replication appears to be relatively low and the data do not suggest high frequencies of replication errors. However, substantial rearrangements of the AAV genome have been described during lytic infection leading to the formation of defective interfering particles. Irrespective of the mechanisms that lead to sequence divergence, with few exceptions, vp1 structures of the quasispecies remained intact without frameshifts or nonsense mutations suggesting that competitive selection of viruses with the most favorable profile of fitness contribute to the population

dynamics.

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[0088] These studies have implications in several areas of biology and medicine. The concept of rapid virus evolution, formerly thought to be a property restricted to RNA viruses, should be considered in DNA viruses, which classically have been characterized by serologic assays. It will be important in terms of parvoviruses to develop a new method for describing virus isolates that captures the complexity of its structure and biology, such as with HIV, which are categorized as general families of similar structure and function called Clades. An alternative strategy is to continue to categorize isolates with respect to serologic specificity and develop criteria for describing variants within serologic groups.

Example 3: Vectorology of recombinant AAV genomes equipped with AAV2 ITRs using chimeric plasmids containing AAV2 rep and novel AAV cap genes for scrological and gene transfer studies in different animal models.

[0089] Chimeric packaging constructs are generated by fusing AAV2 rep with cap sequences of novel AAV serotypes. These chimeric packaging constructs are used, initially, for pseudotyping recombinant AAV genomes carrying AAV2 ITRs by triple transfection in 293 cell using Ad5 helper plasmid. These pseudotyped vectors are used to evaluate performance in transduction-based serological studies and evaluate gene transfer efficiency of novel AAV serotypes in different animal models including NHP and rodents, before intact and infectious viruses of these novel serotypes are isolated.

### A. pAAV2GFP

[0090] The AAV2 plasmid which contains the AAV2 ITRs and green fluorescent protein expressed under the control of a constitutitive promoter. This plasmid contains the following elements: the AAV2 ITRs, a CMV promoter, and the GFP coding sequences.

### B. Cloning of trans plasmid

[0091] To construct the chimeric trans-plasmid for production of recombinant pseudotyped AAV7 vectors, p5E18 plasmid (Xiao et al., 1999, J. Virol 73:3994-4003) was partially digested with Xho I to linearize the plasmid at the Xho I site at the position of 3169 bp only. The Xho I cut ends were then filled in and ligated back. This modified p5E18 plasmid was restricted with Xba I and Xho I in a complete digestion to remove the AAV2 cap gene sequence and replaced with a 2267 bp Spe I/Xho I fragment containing the AAV7 cap gene which was isolated from pCRAAV7 6-5+15-4 plasmid. [0092] The resulting plasmid contains the AAV2 rep sequences for Rep78/68 under the control of the AAV2 P5 promoter, and the AAV2 rep sequences for Rep52/40 under the control of the AAV2 P19 promoter. The AAV7 capsid sequences are under the control of the AAV2 P40 promoter, which is located within the Rep sequences. This plasmid further contains a spacer 5' of the rep ORF.

### C. Production of Pseudotyped rAAV

[0093] The rAAV particles (AAV2 vector in AAV7 capsid) are generated using an adenovirus-free method. Briefly, the cis plasmid (pAAV2.1 lacZ plasmid containing AAV2 ITRs), and the trans plasmid pCRAAV7 6-5+15-4 (containing the AAV2 rep and AAV7 cap) and a helper plasmid, respectively, were simultaneously co-transfected into 293 cells in a ratio of 1:1:2 by calcium phosphate precipitation.

[0094] For the construction of the pAd helper plasmids, pBG 10 plasmid was purchased from Microbix (Canada). A RsrII fragment containing L2 and L3 was deleted from pBHG10, resulting in the first helper plasmid, pAd $\Delta$ F13. Plasmid Ad $\Delta$ F1 was constructed by cloning Asp700/SalI fragment with a Pmel/Sgfl deletion, isolating from pBHG10, into Bluescript. MLP, L2, L2 and L3 were deleted in the pAd $\Delta$ F1. Further deletions of a 2.3 kb NruI fragment and, subsequently, a 0.5 kb RsrII/NruI fragment generated helper plasmids pAd $\Delta$ F5 and pAd $\Delta$ F6, respectively. The helper plasmid, termed p $\Delta$ F6, provides the essential helper functions of E2a and E4 ORF6 not provided by the E1-expressing helper ceII, but is deleted of adenoviral capsid proteins and functional E1 regions).

[0095] Typically, 50 μg of DNA (cis:trans:helper) was transfected onto a 150 mm tissue culture dish. The 293 cells were harvested 72 hours post-transfection, sonicated and treated with 0.5% sodium deoxycholate (37°C for 10 min.) Cell lysates were then subjected to two rounds of a CsCl gradient. Peak fractions containing rAAV vector are collected, pooled and dialyzed against PBS.

Example 4: Creation of infectious clones carrying intact novel AAV serotypes for study of basic virology in human and NHP derived cell lines and evaluation of pathogenesis of novel AAV serotypes in NHP and other animal models.

[0096] To achieve this goal, the genome walker system is employed to obtain 5' and 3' terminal sequences (ITRs)

and complete construction of clones containing intact novel AAV serotype genomes.

[0097] Briefly, utilizing a commercially available Universal Genome Walker Kit [Clontech], genomic DNAs from monkey tissues or cell lines that are identified as positive for the presence of AAV7 sequence are digested with Dra I, EcoR V, Pvu II and Stu I endonucleases and ligated to Genome Walker Adaptor to generate 4 individual Genome Walker Libraries (GWLs). Using DNAs from GWLs as templates, AAV7 and adjacent genomic sequences will be PCR-amplified by the adaptor primer 1 (API, provided in the kit) and an AAV7 specific primer 1, followed by a nested PCR using the adaptor primer 2 (AP2) and another AAV7 specific primer 2, both of which are internal to the first set of primers. The major PCR products from the nested PCR are cloned and characterized by sequencing analysis.

[0098] In this experiment, the primers covering the 257 bp or other signature fragment of a generic AAV genome are used for PCR amplification of cellular DNAs extracted from Human and NHP derived cell lines to identify and characterize latent AAV sequences. The identified latent AAV genomes are rescued from the positive cell lines using adenovirus helpers of different species and strains.

[0099] To isolate infectious AAV clones from NHP derived cell lines, a desired cell line is obtained from ATCC and screened by PCR to identify the 257 bp amplicon, i.e., signature region of the invention. The 257 bp PCR product is cloned and serotyped by sequencing analysis. For these cell lines containing the AAV7 sequence, the cells are infected with SV-15, a simian adenovirus purchased from ATCC, human Ad5 or transfected with plasmid construct housing the human Ad genes that are responsible for AAV helper functions. At 48 hour post infection or transfection, the cells are harvested and Hirt DNA is prepared for cloning of AAV7 genome following Xiao et al., 1999, J. Virol, 73:3994-4003.

### Example 5 - Production of AAV Vectors

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[0100] A pseudotyping strategy similar to that of Example 3 for AAV1/7 was employed to produce AAV2 vectors packaged with AAV1, AAV5 and AAV8 capsid proteins. Briefly, recombinant AAV genomes equipped with AAV2 ITRs were packaged by triple transfection of 293 cells with cis-plasmid, adenovirus helper plasmid and a chimeric packaging construct where the AAV2 rep gene is fused with cap genes of novel AAV serotypes. To create the chimeric packaging constructs, the Xho I site of p5E18 plasmid at 3169 bp was ablated and the modified plasmid was restricted with Xba I and Xho I in a complete digestion to remove the AAV2 cap gene and replace it with a 2267 bp Spe I/Xho I fragment containing the AAV8 cap gene [Xiao, W., et al., (1999) J Virol 73, 3994-4003]. A similar cloning strategy was used for creation of chimeric packaging plasmids of AAV2/1 and AAV2/5. All recombinant vectors were purified by the standard CsCl<sub>2</sub> sedimentation method except for AAV2/2, which was purified by single step heparin chromatography.

[0101] Genome copy (GC) titers of AAV vectors were determined by TaqMan analysis using probes and primers targeting SV40 poly A region as described previously [Gao, G., et al., (2000) *Hum Gene Ther* 11, 2079-91].

[0102] Vectors were constructed for each serotype for a number of *in vitro* and *in vivo* studies. Eight different transgene cassettes were incorporated into the vectors and recombinant virions were produced for each serotype. The recovery of virus, based on genome copies, is summarized in Table 4 below. The yields of vector were high for each serotype with no consistent differences between serotypes. Data presented in the table are average genome copy yields with standard deviation x 10<sup>13</sup> of multiple production lots of 50 plate (150 mm) transfections.

Table 4 Production of Recombinant Vectors

	Table 4. Floudction of Recombinant Vectors										
	AAV2/1	AAV2/2	AAV2/5	AAV2/7	AAV2/8						
CMV LacZ	7.30 ± 4.33 (n=9)	4.49 ± 2.89 (n=6)	5.19 ± 5.19 (n=8)	3.42 (n=1)	0.87 (n=1)						
CMV EGFP	6.43 ± 2.42 (n=2)	3.39 ± 2.42 (n=2)	5.55 ± 6.49 (n=4)	2.98 ± 2.66 (n=2)	3.74 ± 3.88 (n=2)						
TBG LacZ	4.18 (n=1)	0.23 (n=1)	0.704 ± 0.43 (n=2)	2.16 (n=1)	0.532 (n=1)						
Alb A1AT	4.67 ± 0.75 (n=2)	4.77 (n=1)	4.09 (n=1)	5.04 (n=1)	2.02 (n=1)						
CB A1AT	0.567 (n=1)	0.438 (n=1)	2.82 (n=1)	2.78 (n=1)	0.816 ± 0.679 (n=2)						
TBG rhCG	8.51 ± 6.65 (n=6)	3.47 ± 2.09 (n=5)	5.26 ± 3.85 (n=4)	6.52 ± 3.08 (n=4)	1.83 ± 0.98 (n=5)						
TBG cFIX	1.24 ± 1.29 (n=3)	0.63 ± 0.394 (n=6)	3.74 ± 2.48 (n=7)	4.05 (n=1)	15.8 ± 15.0 (n=5)						

Example 6 - Serologic Analysis of Pseudotyped Vectors

[0103] C57BL/6 mice were injected with vectors of different serotypes of AAVCBA1AT vectors intramuscularly (5 x

10<sup>11</sup> GC) and serum samples were collected 34 days later. To test neutralizing and cross-neutralizing activity of sera to each serotype of AAV, sera was analyzed in a transduction based neutralizing antibody assay [Gao, G. P., et al., (1996) *J Virol* 70, 8934-43]. More specifically, the presence of neutralizing antibodies was determined by assessing the ability of serum to inhibit transduction of 84-31 cells by reporter viruses (AAVCMVEGFP) of different serotypes. Specifically, the reporter virus AAVCMVEGFP of each serotype [at multiplicity of infection (MOI) that led to a transduction of 90% of indicator cells] was pre-incubated with heat-inactivated serum from animals that received different serotypes of AAV or from naïve mice. After 1-hour incubation at 37° C, viruses were added to 84-31 cells in 96 well plates for 48 or 72- hour, depending on the virus serotype. Expression of GFP was measured by Fluorolmagin (Molecular Dynamics) and quantified by Image Quant Software. Neutralizing antibody titers were reported as the highest serum dilution that inhibited transduction to less than 50%.

[0104] The availability of GFP expressing vectors simplified the development of an assay for neutralizing antibodies that was based on inhibition of transduction in a permissive cell line (i.e., 293 cells stably expressing E4 from Ad5). Sera to selected AAV serotypes were generated by intramuscular injection of the recombinant viruses. Neutralization of AAV transduction by 1:20 and 1:80 dilutions of the antisera was evaluated (See Table 5 below). Antisera to AAV1, AAV2, AAV5 and AAV8 neutralized transduction of the serotype to which the antiserum was generated (AAV5 and AAV8 to a lesser extent than AAV1 and AAV2) but not to the other serotype (i.e., there was no evidence of cross neutralization suggesting that AAV 8 is a truly unique serotype).

Table 5. Serological Analysis of New AAV Serotypes.

		% Infection on 84-31 cells with AAVCMVEGFP virus:									
		AA	AAV2/1		AAV2/1 AAV2/2 AAV2/5		V2/5	AAV2/7		AAV2/8	
		Serum dilution: Serum dilution: Serum dilutio		dilution:	: Serum dilution:		Serum dilution:				
Sera:	Immunization Vector	1/20	1/80	1/20	1/80	1/20	1/80	1/20	1/80	1/20	1/80
Group 1	AAV2/1	0	0	100	100	100	100	100	100	100	100
Group 2	AAV2/2	100	100	0	0	100	100	100	100	100	100
Group 3	AAV2/5	100′	100	100	100	16.5	16.5	100	100	100	100
Group 4	AAV2/7	100	100	100	100	100	100	61.5	100	100	100
Group 5	AAV2/8	100	100	100	100	100	100	100	.100	26.3	60

[0105] Human sera from 52 normal subjects were screened for neutralization against selected serotypes. No serum sample was found to neutralize AAV2/7 and AAV2/8 while AAV2/2 and AAV2/1 vectors were neutralized in 20% and 10% of sera, respectively. A fraction of human pooled IgG representing a collection of 60,000 individual samples did not neutralize AAV2/7 and AAV2/8, whereas AAV2/2 and AAV2/1 vectors were neutralized at titers of serum equal to 1/1280 and 1/640, respectively.

Example 7 - In vivo Evaluation of Different Serotypes of AAV Vectors

[0106] In this study, 7 recombinant AAV genomes, AAV2CBhAIAT, AAV2AlbhAIAt, AAV2CMVrhCG, AAV2TBGrhCG, AAV2TBGcFIX, AAV2CMVLacZ and AAV2TBGLacZ were packaged with capsid proteins of different serotypes. In all 7 constructs, minigene cassettes were flanked with AAV2 ITRs. cDNAs of human  $\alpha$ -antitrypsin (AIAT) [Xiao, W., et al., (1999) J Virol 73, 3994-4003]  $\beta$ -subunit of rhesus monkey choriogonadotropic hormone (CG) [Zoltick, P. W. & Wilson, J. M. (2000) *Mol Ther* 2, 657-9] canine factor IX [Wang, L., et al., (1997) *Proc Natl Acad Sci USA* 94, 11563-6] and bacterial  $\beta$ -glactosidase (i.e., Lac Z) genes were used as reporter genes. For liver-directed gene transfer, either mouse albumin gene promoter (Alb) [Xiao, W. (1999), cited above] or human thyroid hormone binding globulin gene promoter (TBG) [Wang (1997), cited above] was used to drive liver specific expression of reporter genes. In muscle-directed gene transfer experiments, either cytomegalovirus early promoter (CMV) or chicken  $\beta$ -actin promoter with CMV enhancer (CB) was employed to direct expression of reporters.

[0107] For muscle-directed gene transfer, vectors were injected into the right tibialis anterior of 4-6 week old NCR nude or C57BL/6 mice (Taconic, Germantown, NY). In liver-directed gene transfer studies, vectors were infused intraportally into 7-9 week old NCR nude or C57BL/6 mice (Taconic, Germantown, NY). Serum samples were collected intraorbitally at different time points after vector administration. Muscle and liver tissues were harvested at different time points for cryosectioning and Xgal histochemical staining from animals that received the lacZ vectors. For the re-administration experiment, C56BL/6 mice initially received AAV2/1, 2/2, 2/5, 2/7 and 2/8CBAIAT vectors intramuscularly and followed for A1AT gene expression for 7 weeks. Animals were then treated with AAV2/8TBGcFIX intraportally and studied for cFIX gene expression.

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[0108] ELISA based assays were performed to quantify serum levels of hA1AT, rhCG and cFIX proteins as described previously [Gao, G. P., et al., (1996) *J Virol* 70, 8934-43; Zoltick, P. W. & Wilson, J. M. (2000) *Mol Ther* 2, 657-9; Wang, L., et al., *Proc Natl Acad Sci U S A* 94, 11563-6]. The experiments were completed when animals were sacrificed for harvest of muscle and liver tissues for DNA extraction and quantitative analysis of genome copies of vectors present in target tissues by TaqMan using the same set of primers and probe as in titration of vector preparations [Zhang, Y., et al., (2001) *Mol Ther* 3, 697-707].

[0109] The performance of vectors base on the new serotypes were evaluated in murine models of muscle and liver-directed gene transfer and compared to vectors based on the known serotypes AAV1, AAV2 and AAV5. Vectors expressing secreted proteins (alpha-antitrypsin (A1AT) and chorionic gonadotropin (CG)) were used to quantitate relative transduction efficiencies between different serotypes through ELISA analysis of sera. The cellular distribution of transduction within the target organ was evaluated using lacZ expressing vectors and X-gal histochemistry.

[0110] The performance of AAV vectors in skeletal muscle was analyzed following direct injection into the tibialis anterior muscles. Vectors contained the same AAV2 based genome with the immediate early gene of CMV or a CMV enhanced β-actin promoter driving expression of the transgene. Previous studies indicated that immune competent C57BL/6 mice elicit limited humoral responses to the human A1AT protein when expressed from AAV vectors [Xiao, W., et al., (1999) *J Virol* 73, 3994-4003].

[0111] In each strain, AAV2/1 vector produced the highest levels of A I AT and AAV2/2 vector the lowest, with AAV2/7 and AAV2/8 vectors showing intermediate levels of expression. Peak levels of CG at 28 days following injection of nu/nu NCR mice showed the highest levels from AAV2/7 and the lowest from AAV2/2 with AAV2/8 and AAV2/1 in between. Injection of AAV2/1 and AAV2/7 lacZ vectors yielded gene expression at the injection sites in all muscle fibers with substantially fewer lacZ positive fibers observed with AAV2/2 and AAV 2/8 vectors. These data indicate that the efficiency of transduction with AA V2/7 vectors in skeletal muscle is similar to that obtained with AAV2/1, which is the most efficient in skeletal muscle of the previously described serotypes [Xiao, W. (1999), cited above; Chao, H., et al., (2001) *Mol Ther* 4, 217-22; Chao, H., et al., (2000) *Mol Ther* 2, 619-23].

[0112] Similar murine models were used to evaluate liver-directed gene, transfer. Identical doses of vector based on genome copies were infused into the portal veins of mice that were analyzed subsequently for expression of the transgene. Each vector contained an AAV2 based genome using previously described liver-specific promoters (i.e., albumin or thyroid hormone binding globulin) to drive expression of the transgene. More particularly, CMVCG and TBGCG minigene cassettes were used for muscle and liver-directed gene transfer, respectively. Levels of rhCG were defined as relative units (RUs x 10³). The data were from assaying serum samples collected at day 28, post vector administration (4 animals per group). As shown in Table 3, the impact of capsid proteins on the efficiency of transduction of A1AT vectors in nu/nu and C57BL/6 mice and CG vectors in C57BL/6 mice was consistent (See Table 6).

Table 6. Expression of β-unit of Rhesus Monkey Chorionic Gonadotropin (rhCG)

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Vector				Muscle	Liver
		AAV2/1		4.5 ± 2.1	1.6 ± 1.0
	•. •	AAV2	•	$0.5 \pm 0.1$	$0.7 \pm 0.3$
		AAV2/5		ND*	$4.8 \pm 0.8$
		AAV2/7		$14.2 \pm 2.4$	$8.2 \pm 4.3$
		AAV2/8		$4.0 \pm 0.7$	$76.0 \pm 22.8$

<sup>\*</sup> Not determined in this experiment.

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[0113] In all cases, AAV2/8 vectors yielded the highest levels of transgene expression that ranged from 16 to 110 greater than what was obtained with AAV2/2 vectors; expression from AAV2/5 and AAV2/7 vectors was intermediate with AAV2/7 higher than AAV2/5. Analysis of X-Gal stained liver sections of animals that received the corresponding lacZ vectors showed a correlation between the number of transduced cells and overall levels of transgene expression. DNAs extracted from livers of C57BL/6 mice who received the A1AT vectors were analyzed for abundance of vector DNA using real time PCR technology.

[0114] The amount of vector DNA found in liver 56 days after injection correlated with the levels of transgene expression (See Table 7). For this experiment, a set of probe and primers targeting the SV40 polyA region of the vector genome was used for TaqMan PCR. Values shown are means of three individual animals with standard deviations. The animals were sacrificed at day 56 to harvest liver tissues for DNA extraction. These studies indicate that AAV8 is the most efficient vector for liver-directed gene transfer due to increased numbers of transduced hepatocytes.

Table 7 - Real Time PCR Analysis for Abundance of AAV Vectors in nu/nu Mouse Liver Following Injection of 1x10<sup>11</sup> Genome Copies of Vector.

AAV vectors/Dose		Genome Copies per Cell
	AAV2/1AlbA1AT	$0.6 \pm 0.36$
	AAV2AlbA1AT	$0.003 \pm 0.001$
	AAV2/5AlbA1AT	$0.83 \pm 0.64$
	AAV2/7AlbA1AT	2.2 ± 1.7
	AAV2/8AlbA1AT	18 ±, 11

[0115] The serologic data described above suggest that AAV2/8 vector should not be neutralized *in vivo* following immunization with the other serotypes. C57BL/6 mice received intraportal injections of AAV2/8 vector expressing canine factor IX ( $10^{11}$  genome copies) 56 days after they received intramuscular injections of A1AT vectors of different serotypes. High levels of factor IX expression were obtained 14 days following infusion of AAV2/8 into naïve animals ( $17\pm2~\mu$ g/ml, n=4) which were not significantly different that what was observed in animals immunized with AAV2/1 ( $31\pm23~\mu$ g/ml, n=4), AAV2/2 ( $16~\mu$ g/ml, n=2), and ÅAV2/7( $12~\mu$ g/ml, n=2). This contrasts to what was observed in AAV2/8 immunized animals that were infused with the AAV2/8 factor IX vector in which no detectable factor IX was observed (<  $0.1~\mu$ g/ml, n=4). [0116] Oligonucleotides to conserved regions of the cap gene did amplify sequences from rhesus monkeys that represented unique AAVs. Identical cap signature sequences were found in multiple tissues from rhesus monkeys derived from at least two different colonies. Full-length rep and cap open reading frames were isolated and sequenced from single sources. Only the cap open reading frames of the novel AAVs were necessary to evaluate their potential as vectors because vectors with the AAV7 or AAV8 capsids were generated using the ITRs and rep from AAV2. This also simplified the comparison of different vectors since the actual vector genome is identical between different vector serotypes. In fact, the yields of recombinant vectors generated using this approach did not differ between serotypes.

[0117] Vectors based on AAV7 and AAV8 appear to be immunologically distinct (i.e., they are not neutralized by antibodies generated against other serotypes). Furthermore, sera from humans do not neutralize transduction by AAV7 and AAV8 vectors, which is a substantial advantage over the human derived AAVs currently under development for which a significant proportion of the human population has pre-existing immunity that is neutralizing [Chirmule, N., et al., (1999) Gene Ther 6, 1574-83].

[0118] The tropism of each new vector is favorable for *in vivo* applications. AAV2/7 vectors appear to transduce skeletal muscle as efficiently as AAV2/1, which is the serotype that confers the highest level of transduction in skeletal muscle of the primate AAVs tested to date [Xiao, W., cited above; Chou (2001), cited above, and Chou (2000), cited above]. Importantly, AAV2/8 provides a substantial advantage over the other serotypes in terms of efficiency of gene transfer to liver that until now has been relatively disappointing in terms of the numbers of hepatocytes stably transduced. AAV2/8 consistently achieved a 10 to 100-fold improvement in gene transfer efficiency as compared to the other vectors. The basis for the improved efficiency of AAV2/8 is unclear, although it presumably is due to uptake via a different receptor that is more active on the basolateral surface of hepatocytes. This improved efficiency will be quite useful in the development of liver-directed gene transfer where the number of transduced cells is critical, such as in urea cycle disorders and familial hypercholesterolemia.

[0119] Thus, the present invention provides a novel approach for isolating new AAVs based on PCR retrieval of genomic sequences. The amplified sequences were easily incorporated into vectors and tested in animals. The lack of pre-existing immunity to AAV7 and the favorable tropism of the vectors for muscle indicates that AAV7 is suitable for use as a vector in human gene therapy and other *in vivo* applications. Similarly, the lack of pre-existing immunity to the AAV serotypes of the invention, and their tropisms, renders them useful in delivery of therapeutic molecules and other useful molecules.

### Example 9 - Tissue Tropism Studies

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[0120] In the design of a high throughput functional screening scheme for novel AAV constructs, a non-tissue specific and highly active promoter, CB promoter (CMV enhanced chicken β actin promoter) was selected to drive an easily detectable and quantifiable reporter gene, human α anti-trypsin gene. Thus only one vector for each new AAV clone needs to be made for gene transfer studies targeting 3 different tissues, liver, lung and muscle to screen for tissue tropism of a particular AAV construct. The following table summarizes data generated from 4 novel AAV vectors in the tissue tropism studies (AAVCBA1AT), from which a novel AAV capsid clone, 44.2, was found to be a very potent gene transfer vehicle in all 3 tissues with a big lead in the lung tissue particularly. Table 8 reports data obtained (in μg A1AT/mL serum) at day 14 of the study.

Table 8

Vector	Target Tissue						
	Lung	Liver	Muscle				
AAV2/1	ND	ND	45±11				
AAV2/5	0.6±0.2	ND	ND				
AAV2/8	ND	84±30	·ND				
AAV2/rh.2 (43.1)	14±7	25±7.4	35±14				
AAV2/rh.10 (44.2)	23±6	53±19	46±11				
AAV2/rh.13 (42.2)	3.5±2	2±0.8	3.5±1.7				
AAV2/rh.21 (42.10)	3.1±2	2±1.4	4.3±2				

A couple of other experiments were then performed to confirm the superior tropism of AAV 44.2 in lung tissue. First, AAV vector carried CC10hA1AT minigene for lung specific expression were pseudotyped with capsids of novel AAVs were given to Immune deficient animals (NCR nude) in equal volume (50  $\mu$ I each of the original preps without dilution) via intratracheal injections as provided in the following table. In Table 9, 50  $\mu$ I of each original prep per mouse, NCR Nude, detection limit  $\geq$ 0.033  $\mu$ g/mI, Day 28

Table 9

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Vector	Total GC in 50 μl vector	µg of A1AT/ml with 50µl vector	μg of A1AT/ml with 1x10 <sup>11</sup> vector	Relative Gene transfer as compared to rh.10 (clone 44.2)
2/1	3x10 <sup>12</sup>	2.6±0.5	0.09±0.02	2.2
2/2	5.5x10 <sup>11</sup>	<0.03	<0.005	<0.1
2/5	3.6x10 <sup>12</sup>	0.65±0.16	0.02=0.004	0.5
2/7	4.2x10 <sup>12</sup>	1±0.53	0.02±0.01	0.5
2/8	7.5x10 <sup>11</sup>	0.9±0.7	0.12±0.09	2.9
2/ch.5 (A.3.1)	9x10 <sup>12</sup>	1±0.7	0.01±0.008	0.24
2/rh.8 (43.25)	4.6x10 <sup>12</sup>	26±21	0.56±0.46	13.7
2/rh.10 (44.2)	2.8x10 <sup>12</sup>	115±38	4.1±1.4	100
2/rh.13 (42.2)	6x10 <sup>12</sup>	7.3±0.8	0.12±0.01	2.9
2/rh.21 (42.10)	2.4x10 <sup>12</sup>	9±0.9	0.38±0.04	9.3
2/rh.22 (42.11)	2.6x10 <sup>12</sup>	6±0.4	0.23±0.02	5.6
2/rh.24 (42.13)	1.1x10 <sup>11</sup>	0.4±0.3	0.4±0.3	1

The vectors were also administered to immune competent animals (C57BL/6) in equal genome copies (1x10<sup>11</sup> GC) as shown in the Table 10. (1x10<sup>11</sup> GC per animal, C57BL/6, day 14, detection limit  $\geq$ 0.033  $\mu$ g/ml)

Table 10

AAV Vector	μg of A1AT/ml with 1x10 <sup>11</sup> vector	Relative Gene transfer as compared to rh.10 (clone 44.2)
2/1	0.076±0.031	2.6
2/2	0.1±0.09	3.4
2/5	0.0840.033	2.9

### Table continued

AAV Vector	μg of A1AT/ml with 1x10 <sup>11</sup> vector	Relative Gene transfer as compared to rh.10 (clone 44.2)
2/7	0.33±0.01	11
2/8	1.92±1.3	2.9
2/ch.5 (A.3.1)	· 0.048±0.004	1.6
2/rh.8 (43.25)	1.7±0.7	58
2/rh.10 (44.2)	2.93±1.7	100
2/巾.13 (42.2)	0.45±0.15	15
2/rh.21 (42.10)	0.86±0.32	29
2/rh.22 (42.11)	0.38±0.18	13
2/rh.24 (42.13)	0.3±0.19	10

[0121] The data from both experiments confirmed the superb tropism of clone 44.2 in lung-directed gene transfer.

[0122] Interestingly, performance of clone 44.2 in liver and muscle directed gene transfer was also outstanding, close to that of the best liver transducer, AAV8 and the best muscle transducer AAV1, suggesting that this novel AAV has some intriguing biological significance.

[0123] To study serological properties of those novel AAVs, pseudotyped AAVGFP vectors were created for immunization of rabbits and in vitro transduction of 84-31 cells in the presence and absence of antisera against different capsids. The data are summarized below:

Table 11a. Cross-NAB assay in 8431 cells and adenovirus (Adv) coinfection in 6431 cells (coinfected with Adv) with:

Serum from rabbit immunized with:	10 <sup>9</sup> GC	10 <sup>9</sup> GC	10 <sup>9</sup> GC	10 <sup>10</sup> GC
	rh.13	rh.21	rh.22	rh.24
	AAV2/42.2	AAV2/42.10	AAV2/42.1	AAV2/42.13
AAV2/1	1/20	1/20	1/20	No NAB
AAV2/2	1/640	1/1280	1/5120	No NAB
AAV2/5	No NAB	1/40	1/160	No NAB
AAV2/7	1/81920	1/81920	1/40960	1/640
AAV2/8	1/640	1/640	1/320	1/5120
Ch.5 AAV2/A3	1/20	1/160	1/640	1/640
<i>rh.8</i> AAV2/43.25	1/20	1/20	1/20	1/320
rh.10 AAV2/44.2	No NAB	No NAB	No NAB	1/5120
rh.13 AAV2/42.2	1/5120	1/5120	1/5120	No NAB
<i>rh.21</i> AA V2/42.10	1/5120	1/10240	1/5120	1/20
<i>rh.22</i> AAV2/42.11	1/20480	1/20480	1/40960	No NAB
<i>rh.24</i> . AAV2/42.13	No NAB	1/20	1/20	1/5120

Table 11b. Cross-NAB assay in 8431 cells and Adv coinfection Infection in 8431 cells (coinfected with Adv) with:

Serum from rabbit immunized with:	10 <sup>9</sup> GC	10 <sup>10</sup> GC	10 <sup>10</sup> GC	10 <sup>9</sup> GC	10 <sup>9</sup> GC
·	rh.12	ch.5	rh. 8	rh.10	rh.20
	AAV2/42.1B	AAV2/A3	AAV2/43.25	AAV2/44.2	AAV2/42.8.2
AAV2/1	No NAB	1/20480	No NAB	1/80	ND
AAV2/2	1/20	No NAB	No NAB	No NAB	ND '
AAV2/5	No NAB	1/320	No NAB	No NAB	ND
AAV2/7	1/2560	1/640	1/160	1/81920	ND
AAV2/8	1/10240	1/2560	1/2560	1/81920	ND
<i>ch.5</i> AAV2/A3	1/1280	1/10240	ND	1/5120	1/320
rh.8 AAV2/43.25	1/1280	ND	1/20400	1/5120	1/2560
rh.10 AAV2/44.2	1/5120	ND	ND	1/5120	1/5120
rh.13 AAV2/42.2	1/20	ND	ND	No NAB	1/320
rh.21 AAV2/42.10	1/20	ND	ND	1/40	1/80
<i>rh.22</i> AAV2/42.1 1	No NAB	ND	ND	ND	No NAB
rh.24 AAV2/42.13	1/5120	ND	ND	ND	1/2560

Table 12

	Titer of rabbit s	Titer after Boosting	
	Vector	Titer d21	
ch.5	AAV2/A3	1/10,240	1/40,960
rh.8	AAV2/43.25	1/20,400	1/163,840
rh.10	AAV2/44.2	1/10,240	1/527,680
rh.13	AAV2/42.2	1/5,120	1/20,960
rh.21	AAV2/42.10	1/20,400	1/81,920
rh.22	AAV2/42.11	1/40,960	ND
rh.24	AAV2/42.13	1/5,120	ND

Table 13 a. Infection in 8431 cells (coinfected with Adv) with GFP

	109 GC/well	10 <sup>9</sup> GC/weli	10 <sup>9</sup> GC/well	10 <sup>9</sup> GC/well	109 GC/well	109 GC/well
						ch.5
	AAV2/1	AAV2/2	AAV2/5	AAV2/7	AAV2/8	AAV2/A3
	128	>200	95	56	13	1
# GFU/field	83	>200	65	54	11	1 '

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		Table 13b. Infec	Table 13b. Infection in 8431 cells (coinfected with Adv) with GFP	ls (coinfected wi	ith Adv) with GF	Ь	•
	109 GC/well	109 GC/well	10 <sup>9</sup> GC/well	109 GC/well	109 GC/well	109 GC/well	109 GC/well
	rh.8	rh. 10	rh.13	rh.21	rh.22	rh.24	rh. 12
	AAV2/43 25	AAV2/44.2	AAV2/43 25 AAV2/44.2 AAV2/42.2 AAV2/42.10 AAV2/42.11 AAV2/42.13 AAV2/42.1B	AAV2/42.10	AAV2/42.11	AAV2/42.13	AAV2/42.1B
	3	13	. 24	62	10	3	18
# GFU/field	2	12 .	7.1	09	14	2	. 20
			48	47	16	3	12
					1		

# Example 10 - Mouse Model of Familial Hypercholesterolemia

[0124] The following experiment demonstrates that the AAV2/7 construct of the invention delivers the LDL receptor and express LDL receptor in an amount sufficient to reduce the levels of plasma cholesterol and triglycerides in animal models of familial hypercholesterolemia.

### A. Vector Construction

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[0125] AAV vectors packaged with AAV7 or AAV8 capsid proteins were constructed using a pseudotyping strategy [Hildinger M, et al., J. Virol 2001; 75:6199-6203]. Recombinant AAV genomes with AAV2 inverted terminal repeats (ITR) were packaged by triple transfection of 293 cells with the *cis*-plasmid, the adenovirus helper plasmid and a chimeric packaging construct, a fusion of the capsids of the novel AAV serotypes with the rep gene of AAV2. The chimeric packaging plasmid was constructed as previously described [Hildinger et al, cited above]. The recombinant vectors were purified by the standard CsCl<sub>2</sub> sedimentation method. To determine the yield TaqMan (Applied Biosystems) analysis was performed using probes and primers targeting the SV40 poly(A) region of the vectors [Gao GP, et al., Hum Gene Ther. 2000 Oct 10;11(15):2079-91]. The resulting vectors express the transgene under the control of the human thyroid hormone binding globulin gene promoter (TBG).

### B. Animals

[0126] LDL receptor deficient mice on the C57Bl/6 background were purchased from the Jackson Laboratory (Bar Harbor, ME, USA) and maintained as a breeding colony. Mice were given unrestricted access to water and obtained a high fat Western Diet (high % cholesterol) starting three weeks prior vector injection. At day -7 as well at day 0, blood was obtained via retroorbital bleeds and the lipid profile evaluated. The mice were randomly divided into seven groups. The vector was injected via an intraportal injection as previously described ([Chen SJ et al., Mol Therapy 2000; 2(3), 256-261]. Briefly, the mice were anaesthetized with ketamine and xylazine. A laparotomy was performed and the portal vein exposed. Using a 30g needle the appropriate dose of vector diluted in 100ul PBS was directly injected into the portal vein. Pressure was applied to the injection site to ensure a stop of the bleeding. The skin wound was closed and draped and the mice carefully monitored for the following day. Weekly bleeds were performed starting at day 14 after liver directed gene transfer to measure blood lipids. Two animals of each group were sacrificed at the time points week 6 and week 12 after vector injection to examine atherosclerotic plaque size as well as receptor expression. The remaining mice were sacrificed at week 20 for plaque measurement and determination oftransgene expression.

Table 14

	Vector	dose	п
Group 1	AAV2/7-TBG-hLDLr	1x 10 <sup>12</sup> gc	12
Group 2	AAV2/7-TBG-hLDLr	3x 10 <sup>11</sup> gc	12
Group 3	AAV2/7-TBG-hLDLr	1x 10 <sup>11</sup> gc	12
Group 4	AAV2/8-TBG-hLDLr	1x 10 <sup>12</sup> gc	12
Group 5	AAV2/8-TBG-hLDLr	3x 10 <sup>11</sup> gc	12
Group 6	AAV2/8-TBG-hLDLr	1x 10 <sup>11</sup> gc	12
Group 7	AAV2/7-TBG-LacZ	1x 10 <sup>11</sup> gc	16

### C. Serum lipoprotein and liver function analysis

[0127] Blood samples were obtained from the retroorbital plexus after a 6 hour fasting period. The serum was separated from the plasma by centrifugation. The amount of plasma lipoproteins and liver transaminases in the serum were detected using an automatized clinical chemistry analyzer (ACE, Schiapparelli Biosystems, Alpha Wassermann)

### D. Detection of transgene expression

[0128] LDL receptor expression was evaluated by immuno-fluorescence staining and Western blotting. For Western Blot frozen liver tissue was homogenized with lysis buffer (20 mM Tris, pH7.4, 130mM NaCl, 1% Triton X 100, proteinase inhibitor (complete, EDTA-free, Roche, Mannheim, Germany). Protein concentration was determined using the Micro

BCA Protein Assay Reagent Kit (Pierce, Rockford, IL). 40 μg of protein was resolved on 4- 15% Tris-HCl Ready Gels (Biorad, Hercules, CA) and transferred to a nitrocellulose membrane (Invitrogen,). To generate Anti-hLDL receptor antibodies a rabbit was injected intravenously with an AdhLDLr prep (1x10<sup>13</sup> GC). Four weeks later the rabbit serum was obtained and used for Western Blot. A 1:100 dilution of the serum was used as a primary antibody followed by a HRP-conjugated anti-rabbit IgG and ECL chemiluminescent detection (ECL Western Blot Detection Kit, Amersham, Arlington Heights, IL).

### E. Immunocytochemistry

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[0129] For determination of LDL receptor expression in frozen liver sections immunohistochemistry analyses were performed. 10um cryostat sections were either fixed in acetone for 5 minutes, or unfixed. Blocking was obtained *via a* 1 hour incubation period with 10% of goat serum. Sections were then incubated for one hour with the primary antibody at room temperature. A rabbit polyclonal antibody anti-human LDL (Biomedical Technologies Inc., Stoughton, MA) was used diluted accordingly to the instructions of the manufacturer. The sections were washed with PBS, and incubated with 1:100 diluted fluorescein goat anti-rabbit IgG (Sigma, St Louis, MO). Specimens were finally examined under fluorescence microscope Nikon Microphot-FXA. In all cases, each incubation was followed by extensive washing with PBS. Negative controls consisted of preincubation with PBS, omission of the primary antibody, and substitution of the primary antibody by an isotype-matched non-immune control antibody. The three types of controls mentioned above were performed for each experiment on the same day.

### F. Gene transfer efficiency

[0130] Liver tissue was obtained after sacrificing the mice at the designated time points. The tissue was shock frozen in liquid nitrogen and stored at -80°C until further processing. DNA was extracted from the liver tissue using a QIAamp DNA Mini Kit (QIAGEN GmbH, Germany) according to the manufacturers protocol. Genome copies of AAV vectors in the liver tissue were evaluated using Taqman analysis using probes and primers against the SV40 poly(A) tail as described above.

### G. Atherosclerotic plaque measurement

[0131] For the quantification of the atherosclerotic plaques in the mouse aorta the mice were anaesthetized (10% ketamine and xylazine, ip), the chest opened and the arterial system perfused with ice-cold phosphate buffered saline through the left ventricle. The aorta was then carefully harvested, slit down along the ventral midline from the aortic arch down to the femoral arteries and fixed in formalin. The lipid-rich atherosclerotic plaques were stained with Sudan IV (Sigma, Germany) and the aorta pinned out flat on a black wax surface. The image was captured with a Sony DXC-960 MD color video camera. The area of the plaque as well as of the complete aortic surface was determined using Phase 3 Imaging Systems (Media Cybernetics).

### H. Clearance of I125 LDL

[0132] Two animals per experimental group were tested. A bolus of I<sup>125</sup>-labeled LDL (generously provided by Dan Rader, U Penn) was infused slowly through the tail vein over a period of 30 sec (1,000,000 counts of [I<sup>125</sup>]-LDL diluted in 100 µl sterile PBS/ animal). At time points 3min, 30 min, 1.5hr, 3hr, 6hr after injection a blood sample was obtained via the retro-orbital plexus. The plasma was separated off from the whole blood and 10 µl plasma counted in the gamma counter. Finally the fractional catabolic rate was calculated from the lipoprotein clearance data.

## I. Evaluation of Liver Lipid accumulation

[0133] Oil Red Staining of frozen liver sections was performed to determine lipid accumulation. The frozen liver sections were briefly rinsed in distilled water followed by a 2 minute incubation in absolute propylene glycol. The sections were then stained in oil red solution (0.5% in propylene glycol) for 16 hours followed by counterstaining with Mayer's hematoxylin solution for 30 seconds and mounting in warmed glycerin jelly solution.

[0134] For quantification of the liver cholesterol and triglyceride content liver sections were homogenized and incubated in chloroform/methanol (2:1) overnight. After adding of  $0.05\%~H_2SO_4$  and centrifugation for 10 minutes, the lower layer of each sample was collected, divided in two aliquots and dried under nitrogen. For the cholesterol measurement the dried lipids of the first aliquot were dissolved in 1% Triton X-100 in chloroform. Once dissolved, the solution was dried under nitrogen. After dissolving the lipids in ddH $_2$ 0 and incubation for 30 minutes at 37°C the total cholesterol concentration was measured using a Total Cholesterol Kit (Wako Diagnostics). For the second aliquot the dried lipids were dissolved

in alcoholic KOH and incubated at 60°C for 30 minutes. Then 1 M MgCl2 was added, followed by incubation on ice for 10 minutes and centrifugation at 14,000 rpm for 30 minutes. The supernatant was finally evaluated for triglycerides (Wako Diagnostics).

[0135] All of the vectors pseudotyped in an AAV2/8 or AAV2/7 capsid lowered total cholesterol, LDL and triglycerides as compared to the control. These test vectors also corrected phenotype of hypercholesterolemia in a dose-dependent manner. A reduction in plaque area for the AAV2/8 and AAV2/7 mice was observed in treated mice at the first test (2 months), and the effect was observed to persist over the length of the experiment (6 months).

Example 10 - Functional Factor IX Expression and Correction of Hemophilia

### A. Knock-Out Mice

[0136] Functional canine factor IX (FIX) expression was assessed in hemophilia B mice. Vectors with capsids of AAV1, AAV2, AAV5, AAV7 or AAV8 were constructed to deliver AAV2 5' ITR - liver-specific promoter [LSP] - canine FIX - woodchuck hepatitis post-regulatory element (WPRE) - AAV2 3' ITR. The vectors were constructed as described in Wang et al, 2000, *Molecular Therapy* 2: 154-158), using the appropriate capsids.

[0137] Knock-out mice were generated as described in Wang et al, 1997. *Proc. Natl. Acad. Sci. USA* 94: 11563-11566. This model closely mimic the phenotypes of hemophilia B in human.

[0138] Vectors of different serotypes (AAV1, AAV2, AAV5, AAV7 and AAV8) were delivered as a single intraportal injection into the liver of adult hemophiliac C57Bl/6 mice in a dose of 1x10<sup>11</sup> GC/mouse for the five different serotypes and one group received an AAV8 vector at a lower dose, 1x10<sup>10</sup> GC/mouse. Control group was injected with 1 x 10<sup>11</sup> GC of AAV2/8 TBG LacZ3. Each group contains 5-10 male and female mice. Mice were bled bi-weekly after vector administration.

### 1. ELISA

[0139] The canine FIX concentration in the mouse plasma was determined by an ELISA assay specific for canine factor IX, performed essentially as described by Axelrod et al, 1990, *Proc.Natl.Acad.Sci. USA*, 87:5173-5177 with modifications. Sheep anti-canine factor IX (Enzyme Research Laboratories) was used as primary antibody and rabbit anti-canine factor IX ((Enzyme Research Laboratories) was used as secondary antibody. Beginning at two weeks following injection, increased plasma levels of cFIX were detected for all test vectors. The increased levels were sustained at therapeutic levels throughout the length of the experiment, i.e., to 12 weeks. Therapeutic levels are considered to be 5% of normal levels, i.e., at about 250 ng/mL.

[0140] The highest levels of expression were observed for the AAV2/8 (at 10<sup>11</sup>) and AAV2/7 constructs, with sustained superphysiology levels cFIX levels (ten-fold higher than the normal level). Expression levels for AAV2/8 (10<sup>11</sup>) were approximately 10 fold higher than those observed for AAV2/2 and AAV2/8 (10<sup>10</sup>). The lowest expression levels, although still above the therapeutic range, were observed for AAV2/5.

### 2. In Vitro Activated Partial Thromboplastin time (aPTT) Assay

[0141] Functional factor IX activity in plasma of the FIX knock-out mice was determined by an *in vitro* activated partial thromboplastin time (aPTT) assay-Mouse blood samples were collected from the retro-orbital plexus into 1/10 volume of citrate buffer. The aPTT assay was performed as described by Wang et al, 1997, *Proc. Natl. Acad. Sci. USA* 94: 11563-11566.

[0142] Clotting times by aPTT on plasma samples of all vector injected mice were within the normal range (approximately 60 sec) when measured at two weeks post-injection, and sustained clotting times in the normal or shorter than normal range throughout the study period (12 weeks).

[0143] Lowest sustained clotting times were observed in the animals receiving AAV2/8 (10<sup>11</sup>) and AAV2/7. By week 12, AAV2/2 also induced clotting times similar to those for AAV2/8 and AAV2/7. However, this lowered clotting time was not observed for AAV2/2 until week 12, whereas lowered clotting times (in the 25 - 40 sec range) were observed for AAV2/8 and AAV2/7 beginning at week two.

[0144] Immuno-histochemistry staining on the liver tissues harvested from some of the treated mice is currently being performed. About 70-80% of hepatocytes are stained positive for canine FIX in the mouse injected with AAV2/8.cFIX vector.

### B. Hemophilia B Dogs

[0145] Dogs that have a point mutation in the catalytic domain of the F.IX gene, which, based on modeling studies.

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appears to render the protein unstable, suffer from hemophilia B [Evans et al, 1989, Proc. Natl. Acad. Sci. USA, 86:10095-10099). A colony of such dogs has been maintained for more than two decades at the University of North Carolina, Chapel Hill. The homeostatic parameters of these dogs are well described and include the absence of plasma F.IX antigen, whole blood clotting times in excess of 60 minutes, whereas normal dogs are 6-8 minutes, and prolonged activated partial thromboplastin time of 50-80 seconds, whereas normal dogs are 13-28 seconds. These dogs experience recurrent spontaneous hemorrhages. Typically, significant bleeding episodes are successfully managed by the single intravenous infusion of 10 ml/kg of normal canine plasma; occasionally, repeat infusions are required to control bleeding. [0146] Four dogs are injected intraportally with AAV.cFIX according to the schedule below. A first dog receives a single injection with AAV2/2.cFIX at a dose of 3.7x10<sup>11</sup> genome copies (GC)/kg. A second dog receives a first injection of AAV2/2.cFIX (2.8x10<sup>11</sup> GC/kg), followed by a second injection with AAV2/7.cFIX (2.3x10<sup>13</sup> GC/kg) at day 1180. A third dog receives a single injection with AAV2/2.cFIX at a dose of 4.6x10<sup>12</sup> GC/kg. The fourth dog receives an injection with AAV2/2.cFIX (2.8x10<sup>12</sup> GC/kg) and an injection at day 99.5 with AAV2/7.cFIX (5x10<sup>12</sup> GC/kg).

[0147] The abdomen of hemophilia dogs are aseptically and surgically opened under general anesthesia and a single infusion of vector is administered into the portal vein. The animals are protected from hemorrhage in the peri-operative period by intravenous administration of normal canine plasma. The dog is sedated, intubated to induce general anesthesia, and the abdomen shaved and prepped. After the abdomen is opened, the spleen is moved into the operative field. The splenic vein is located and a suture is loosely placed proximal to a small distal incision in the vein. A needle is rapidly inserted into the vein, then the suture loosened and a 5 F cannula is threaded to an intravenous location near the portal vein bifurcation. After hemostasis is secured and the catheter balloon inflated, approximately 5.0 ml of vector diluted in PBS is infused into the portal vein over a 5 minute interval. The vector infusion is followed by a 5.0 ml infusion of saline. The balloon is then deflated, the callula removed and venous hemostasis is secured. The spleen is then replaced, bleeding vessels are cauterized and the operative wound is closed. The animal is extubated having tolerated the surgical procedure well. Blood samples are analyzed as described. [Wang et al, 2000, *Molecular Therapy* 2: 154-158]

<sup>25</sup> [0148] Results showing correction or partial correction are anticipated for AAV2/7.

### SEQUENCE LISTING

### [0149]

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<211> 3122

<212> DNA

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<213> new AAV serotype, clone 43.20

<400> 42

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1980

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<211> 3121

<212> DNA

<213> new AAV serotype, clone 43.23

<400> 44

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<400> 46

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<210> 48

<211> 1933

<212> DNA

<213> new AAV serotype, clone 223.10

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<221> misc\_feature

<222> (1302)..(1302)

<223> can be a, c, g or t

<400> 48

<220>

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<211> 1933

<212> DNA

<213> new AAV serotype, clone 223.2

<400> 49

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<211> 1933

<212> DNA

<213> new AAV serotype, clone 223.4

<400> 50

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<213> new AAV serotype, clone 223.6

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ne.											٠					
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4. j. +4+4

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. 30	Leu	Gly 130	Leu	Val	Glu	Glu	Ala 135	Val	Lys	Thr		Pro 140	Gly	Lys	Lys	Arg

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15	Ala	Pro 210		Ala	Ąsp	Asn	Asn 215		Gly	Ala	qeA	Gly 220		Gly	/ Asn	ser .
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רר																

	Asj	p Va	l Pro	420	e His	3 Se.	r Se	r Ty.	r Al 42	а Ні. 5	s Se	r Glr	s Sei	430		p Arg
5	Lei	ı Me	435	Pro	) Lev	Ile	e Asp	Gl: 440	n <b>Ty</b> :	r Lei	и ту:	Tyr	145		Ly.	s Thr
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45																			÷-
50																			

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	Tyr	Val	Leu 275	Gly	Ser	Ala	His	Gln 280	Gly	Cys	Leu	Pro	Pro 285	Phe	Pro	Ala
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25	Ser 305		Ser	Val	GΊΥ	Arg 310	Ser	Ser	Phe	Tyr	Cys 315	Гел	eĵп	Tyr	Phe	Pro 320
	Ser	Gln	Met	Leu	Arg 325	Thr	Gly	Asn	Asn 	Phe 330	Thr	Phe	Ser	Tyr	Thr 335	Phe
30	Glu	Asp	Val	Pro 340	Phe	His	Ser	Ser	Tyr 345	Aļa	His	Ser	Gln	ser 350	Leu	Gly
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		370		Asn			375					380				
	385			Gly		390					395					400
45	Pro	Gly	Pro	Суз	Phe 405	Arg	Gln	Gln	Arg	Val 410	Ser	Lys	Thr	Leu	Asp 415	Gln
· · · · · · · · · · · · · · · · · · ·	Asn	Asn	Asn	Ser 420	Asn	Phe	Ala	Trp	Thr 425	Gly	Ala	Thr	Lys	Tyr 430	His	Leu
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		Thr		GJ <i>n</i>	G1u	Glu 485	Ile	Arg	Pro	Thr	Asn 490	Pro	Val	Ala	Thr	Glu 495	G]π
10		Tyr			Val 500	Ser	Ser	Asn	Leu	Gln 505	Ala	Ala	Ser	Thr	Ala 510	Ala	Gln
15		Thr	Gln	Val 515		Asn	Asn	Gln	Gly 520	Ala	Leu	Pro	Gly	Met 525	Val	Trp	Gln
		Asn	Arg 530	Ąsp	Val	Tyr	Leu	Gln 535	Gly	Pro	Ile	Trp	Ala 540	Lys	Ile	Pro	His
20		Thr 545	Asp	Gly	Asn		His 550	Pro	Ser	Pro	Leu	Met 555	Gly	eīà	Phe	Gly	Leu 560
25		Lys	His	Pro	Pro	565	Gln	Ilė	Leu	Ile	Lys 570	Asn	Thr	Pro	Val	Pro 575	Ala
		Asn	Pro	Pro	Glu 580	Val	Phe	Thr	Pro	Ala 585	Lys	Phe	Ala	Ser	Phe 590	Ile	Thr
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		Phe 625	Asp	Lys	Gln	Thr	Gly 630	Val	Asp	Phe	Ala	Va1 635	Asp	Ser	Gln	Gly	Val 640
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10	٠.	Ser	Phe	Gly 35	Gly	Asn	Leu	Gly	Arg 40	Ala	Val	Phe ,	Gln	Ala 45	Lys	Lys	Arg
15																	
20																	
25																	
30																	
35																	
40																	
45																	
50	,																
55																	

Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly 65  Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr 85  Gly Asp Ser Glu Pro Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro 100  Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly 115  Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly 115  Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala 130  Ser Gly Asn Trp His Cys Asp Ser Thr Arg Leu Gly Asp Arg Val Ile 145  Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu 160  Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val 180  Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe 195  His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Asn 210  Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln 225  Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro 270  Tyr Val Leu Gly Ser Ala His Gly Cly Cyr Val Thr Thr Ile Ala Asn Asn 245  Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro 270  Tyr Val Leu Gly Ser Ala His Gly Cyr Val Dyn Dan Asn Cyr Cyr Val Leu Fro 270  Tyr Val Leu Gly Ser Ala His Gly Cyr Val Dyn Dyn Dyn Dyn Cyr Cyr Cyr Val Leu Fro 270	5	Vē	al Le 50	eu G]	lu Pr	o Le	u Gl	y Le 55	u Va	l Gl	u Th	r Pr	60	a Ly	s Th	r Al	a Pr
Gly Asp Ser Glu Pro Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro 100 115 Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly 115 Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly Gly 115 135 130 Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala 130 Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala 130 Asn Trp His Cys Asp Ser Thr Arg Leu Gly Asp Arg Val Ile 145 155 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu 165 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu 170 Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val 186 Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe 195 Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Asn Asn 210 Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln 225 Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro 265 Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro 270 Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Pro Pro Ala 275 Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly 280 Nal Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly	3	G1 65	y Ly	s Ly	's Ar	g Pr	0 Va 70	l As	p Se	r Pro	o Ası	9 Se	r Thi	r Se	r Gl	y Il	
Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly 115  Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly 125  Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala 130  Ser Gly Asn Trp His Cys Asp Ser Thr Arg Leu Gly Asp Arg Val Ile 145  Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu 170  Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val 180  Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe 195  His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn 220  Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln 225  Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn 245  Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro 270  Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala 285  Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly	10	Ly	's Ly	s Gl	y Gl	n Gli 85	n Pr	o Ala	a Ly:	s Lys	a Arg	, Leu	reA ı	n Phe	e Gl		n Thi
Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly 115	15	Gl	у Аз	p Se	r Gli 100	Pro	Va:	l Pro	geA o	Pro 105	Gln	Pro	lle	: Gl			o Pro
Ser Gly Asn Trp His Cys Asp Ser Thr Arg Leu Gly Asp Arg Val Ile 145  Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu 175  Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val 180  Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe 195  His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Asn 210  Trp Gly Phe Arg Pro Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln 225  Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn 255  Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro 265  Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala 285  Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly		Ala	a Gl	y Pro	o Ser 5	: Gly	Let	ı Gly	7 Ser 120	Gly	Thr	Met	Ala			y Gly	y Gly
The The Ser The Arg The Trp Ala Leu Pro The Tyr Asn Asn His Leu 175  Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser The Asn Asn Arg Phe 185  Tyr Phe Gly Tyr Ser The Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe 195  His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Asn 2210  Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln 225  Val Lys Glu Val The The Asn Asp Gly Val The The Ile Ala Asn Asn 245  Leu The Ser The Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro 270  Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala 280  Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu The Leu Asn Asn Gly	20	Ala	130	Me1	Ala	qsA	Asn	Asn 135	Glu	Gly	Ala	Asp	Gly 140	Val	. Gly	/ Asr	Ala
Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val 180  Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe 205  His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Asn Gly Val Leu Asn Asn Gly Phe Asp Val 220  Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln 240  Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn 255  Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro 260  Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly	25	Ser 145	Gly	Asr	Trp	His	Cys 150	qeA	Ser	Thr	Arg	Leu 155	Gly	qeA	Arg	Val	
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Ash Arg Phe 195  His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Ash Ash Ash Ash 210  Trp Gly Phe Arg Pro Lys Lys Leu Ash Phe Lys Leu Phe Ash Ile Gln 225  Val Lys Glu Val Thr Thr Ash Asp Gly Val Thr Thr Ile Ala Ash Ash 245  Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro 260  Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala 280  Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Ash Ash Gly		Thr	Thr	Ser	Thr	Arg 165	Thr	Trp	Ala	Leu	Pro 170	Thr	Tyr	neA	Asn		
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn  Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln  225  Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn  255  Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro  260  Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala  285  Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly	30	Tyr	Lys	Gln	Ile 180	Ser	Ser	Gln	Ser	Ala 185	GΊγ	Ser	Thr	Asn			Val
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Asn 210  Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln 225  Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn 255  Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro 270  Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala 285  Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly	35	Tyr	Phe	Gly 195	Tyr	Ser	Thr	Pro	Trp 200	Gly	Tyr	Phe	qeA		ae <b>A</b>	Arg	Phe
Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn 255  Leu Thr Ser Thr Val Gln Val Fhe Ser Asp Ser Glu Tyr Gln Leu Pro 260  Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala 285  Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly		His	Cys 210	His	Phe	Ser	Pro	Arg 215	Asp	Trp	Gln	Arg	Leu 220	Ile	Asn	Asn	Asn
Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro 260  Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala 275  Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly	40	Trp 225	Gly	Phe	Arg	Pro	Lys 230	Lys	Leu	Asn	Phe	Lys 235	Leu	Phe	Asn	Ile	
Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro 260  Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala 275  Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly	45	Val	Lys	Glu	Val	Thr 245	Thr	Asn	Asp	Gly	Val ' 250	Thr	Thr	Ile	Ala		Asn
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly	.•	Leu	Thr	Ser	Thr 260	Val	Gln	Val	Phe	Ser 2 265	Asp :	Ser (	slu '			Leu	Pro
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly	50	Tyr	Val	Leu 275	Gly	Ser 2	Ala	His	Gln ( 280	Gly (	Cys I	Leu 1			Phe	Pro	Ala
		qeA	Val 290	Phe	Met	Ile :	Pro	Gln : 295	Tyr	Gly 7	Tyr I			Leu i	Asn.	Asn	Gly

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10	Glu	qeA	Val	Pro 340		His	Ser	Ser	Tyr 345		His	Ser	·Gln	Ser 350		Gly
15	Arg	Leu	Met 355	Asn	Pro	Leu	Ile	Asp 360	Gln	Tyr	Leu	Tyr	Tyr 365	Leu	Ala	Arg
	Thr	Gln 370	Ser	Asn	Ala	Gly	Gly 375	Thr	Ala	Gly	Asn	Arg 380	Glu	Leu	Gln	Phe
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25	Pro	Gly	Pro	Суз	Phe 405	-	Gln	Gln	Arg	Val 410	Ser	Lys	Thr	Leu	Asp 415	Gln
	aeA	Asn	Asn	Ser 420	Asn	Phe	Ala	Trp	Thr 425	Gly	Ala	Thr	Lys	Tyr 430	His	Leu
30	Asn	Gly	Arg 435		Ser	Leu	Val	Asn 440	Pro	Сĵу	Val	Ala	Met 445	Ala	Thr	His
<i>35</i>	Lys	Asp 450	Asp	Glu	Glu	Arg	Phe 455	Phe	Pro	Ser	Ser	Gly 460	Val	Leu	Ile	Phe
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50	Asn	Arg 530	qeA	Val	Tyr	Leu	Gln 535	Gly	Pro	Ile	Trp	Ala 540	Lys	Ile	Pro	His
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		Ly	s Hi	s Pr	o Pr	565		n Il	e Le	u Il	E Lys 570		n Th	r Pr	o Va	1 Pr 57	o Ala 5
5		Ası	n Pro	o Pr	0 Gl: 580	u Val	Phe	e Th	r Pr	585		Phe	a Ala	a Se	r Ph 59		e Thr
10		Glr	ту:	5 Se.	Thi	Gly	Glr	n Vaļ	L Sei 600		Glu	Ile	e Glu	60:		u Le	u Gln
		Lys	610	L Ası	n Ser	Lys	Arg	Trp 615	Asr	n Pro	Glu	Ile	Glr 620		Th	r Se	r Asn
15		Phe 625	Asp	Lys	Gln	Thr	630	Val	qeA .	Phe	Ala	Val 635	Asp	Ser	Glr	, el	7 Val 640
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		Ser	Phe	Gly 35	Gly	Asn	Leu	Gly	Arg 40	Ala	Val	Phe	Gln	Ala 45	Lys	Lys	Arg
45		Val	Leu 50	Glu	Pro	Leu	Gly	Leu 55	Val	Glu	Thr		Ala 60	Lys	Thr	Ala	Pro
						Dra 1	Va ì	Asn	Ser	Pro	Asp :	Ser '	Thr	Ser	G) v	Tle	C1
50	,	Gly 65	Lys	Lys	Arg		70	, iop				75			,	116	80 .
50	,				Gln		70			Lys .	•	75				Gln 95	80

5	Ala	ı Gly	Pro 115		: Gly	/ Leu	Gly	Ser 120		Thi	. Met	Ala	Ala 125		, el?	A CJA
	Ala	130		: Ala	Asp	Asn	135		Gly	/ Ala	Asp	Gly 140		Gly	Asr	Ala
10	Ser 145		Asn	Trp	His	Cys 150		Ser	Thr	Trp	Leu 155		Asp	Arg	Val	. Ile 160
15	Thr	Thr	Ser	Thr	Arg 165		Trp	Ala	Leu	Pro 170		Tyr	Asn	Asn	His 175	Leu
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25	His	Cys 210	His	Phe	Ser	Pro	Arg 215	<b>Asp</b>	Trp	Gln	Arg	Leu 220	Ile	neA	Asn	neA
	Trp 225	Gly.	Phe	Arg	Pro	Lys 230	Lys	Leu	Asn	Phe	Lys 235	Leu	Бре	neA	Ile	Gln 240
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35	Leu	Thr	Ser	Thr 260	Val	Gln	Val	Phe	Ser 265	Asp	Ser	Glu	Tyr	Gln 270	Leu	Pro
	Tyr	Val	Leu 275	Gly	Ser	Ala	His	Gln 280	Gly	Суз	Leu	Pro	Pro 285	Phe	Pro	Ala
40	qeA	Val 290	Phe	Met	Ile	Pro	Gln 295	Tyr	Gly	Tyr	Leu	Thr 300	Leu	Asn	nzA	Gly
45	ser 305	Gln	Ser	Val	Gly	Arg 310	Ser	Ser	Phe	Tyr	Cys 315	Leu	<b>Gl</b> u	Tyr	Phe	Pro 320
	Ser	Gln	Met	Leu .	Arg 325	Thr	Gly	Asn	Asn	Phe 330	Thr	Phe	Ser	Tyr	Thr 335	Phe
- ,	Glu	Ąsp	Val	Pro 340	Phe	His	Ser		Tyr 345	Ala	His:	Ser		Ser 350	Leu	Asp
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		Tyr 385		Gly	Gly	Pro	390		Met	Ala	. Glu	Gln 395		Lys	neA	Trp	400
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		Thr	Asn	Glu	Glu	Glu 485	Ile	Arg	Pro	Thr	Asn 490	Pro	Val	Ala	Thr	Glu 495	Glu
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		Asn	Arg 530	Asp	Val	Tyr	Leu	Gln 535	Gly	Pro	Ile	Trp	Ala 540	Lys	Ile	Pro	His
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	·	Asn	Pro	Pro	Glu 580	Val	Phe	Thr	Pro	Ala 585	Lys	Phe	Ala	Ser	Phe 590	Ile	Thr
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55		Lys	Glu 610	Asn	Ser	Lys		Trp 615	neA	Pro	Glu	Ile	Gln 620	Tyr	Thr	Ser	neA

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25 ·				35	_		Leu		40					45		-	
		•	50				Gly	55					60				
30		65					Val 70					75					80
35						85	Pro				90					95	
					ioo		Val			105					110		
40				115			Leu		120					125		_	_
45			130				Asn	135					140				
		145		•			Cys 150					155					160
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		Tyr	Phe	Gly 195	Tyr	9er	Thr	Pro	Trp 200	Gly	Tyr	Phe	qeA	Phe 205	Asn	Arg	Phe

5	Hi	210	His	Phe	s Sei	r Pro	215		Trp	Glr	Arg	220		: Asr	reA a	Asn
Y	Tr; 225	el <sup>2</sup>	Phe	Arg	Pro	230		Leu	Asr	n Phe	Lys 235		Phe	e Asr	lle	Gln 240
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	Tyr	Val	Leu 275	Gly	Ser	Ala	His	Gln 280		Суз	Leu	Pro	Pro 285	Phe	Pro	Ala
20	qeA	Val 290	Phe	Met	Ile	Pro	Gln 295	Tyr	Gly	Tyr	Leu	Thr 300	Leu	пеA	Asn	Gly
25 ,	Ser 305	GJW	Ser	Val	Gly	Arg 310	Ser	Ser	Phe	Tyr	Cys 315	Leu	Glu	Tyr	Phe	Pro 320
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		Asn	Arg 530		Val	Tyr	Leu	<b>Gln</b> 535	Gly	Pro	Ile	Trp	Ala 540	Lys	Ile	Pro	His
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5	Se	r Pne	35	, етл	Asn	ı Lei	ı er?	40	, Ale	A VAI	. Phe	GII	45	Lys	з гуз	Arg
	Va	1 Lev 50	ı Glu	Pro	Leu	Gly	, Leu 55	Val	Glu	Thr	Pro	Ala 60	ı Lys	Thr	Ala	Pro
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15	Lys	s Lys	Gly	Gln	61n	Pro	Ala	Lys	Lys	Arg 90	Leu	Asn	Phe	Gly	Gln 95	Thr
	G17	qeA y	Ser	Glu 100	Ser	Val	Pro	Asp	Pro 105		Pro	Ile	Gly	Glu 110		Pro
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	As	p Va 29	l Ph	e Me	t Ile	e Pr	o G1: 29	n Ty 5	r Gl	у Ту	r Le	30		u Asr	a As	n Gly
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	Gli	ı Ası	Val	Pro 340	Phe	His	s Ser	Ser	7 Tyr 345	= Ala	. His	Ser	e Glr	Ser 350		Asp
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E E																

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10		Asr	n Pro	) Šr	580	Va:	l Phe	Th.	r Pro	58:	a Ly. 5	s Il	e Al	a Se	r Ph 59		e Thr
		Gln	Туг	595	Thr	Gly	/ Glm	va:	1 Se: 600	val	l Gl	u Il	e Gl	u Tr 60		u Le	ı Gln
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		Lys	Ala	Asn 35	Gln	Gln	. Lys	Gln	Asp 40	Asp	eJà	Arg	Gly	Leu 45		Leu	Pro
25	• • •	ejÄ	Tyr 50	Lys	Tyr	Leu	Gly	Pro 55	Phe	Asn	Gly	Leu	Asp 60	Lys	Gly	Glu	Pro
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•	Gln	Phe	Glu .	Asp \ 420	/al 1	Pro 1	Phe 1	His S	Ser S 125	Ser :	fyr J	Ala E	His S	Ber G	in s	Ser
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		G1	y Al 21	a Pr .0	o Me	t Al	a As	p As 21	n As 5	n Gl	u Gl	y Al	a As 22		y Va	l Gl	y Se
<i>5</i>		Se 22	r Se	r Gl	y As	n Tr	р Ні 23	s Су 0	s As	p Se	r Th	r Tr 23	p Le	u Gl	y As	p Ar	g Va. 24
10	s	Il	e Th	r Th	r Se	r Th. 24	r Ar	g Th	r Tr	P Al	a Lei 251	u Pro	o Th	r Ty	r As	n As: 25:	
15		Le	u Ty	r Ly	s Glr 260	n Ile	e Se	r Ası	o Gly	7 Th: 26	r Sei	c Gly	y Gly	y Sei	Th. 27	r Ası	a Ası
15		reA	n Thi	27!	r Phe	G13	у Туг	s Ser	280	Pro	Tr	Gly	Tyr	285		Phe	≙ Asr
20		Arg	290	e His	s Cys	His	Phe	295	Pro	Arg	, Asp	Trp	Gln 300	Arg	Let	ı Ile	: Asn
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		Gln.	Phe	Glu	Asp 420	Val	Pro	Phe	His .	Ser 425	Ser	Tyr .	Ala		Ser 430	Gln	Ser
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55	;	Ser	Arg 450	Thr	Gln :	Ser	Thr	Gly ( 455	Gly :	Phr :	Ala (		Thr (	Gln (	Gln	Leu	Leu

	Pr 46	ne Se 55	r Gl	LA a	a Gl	y Pr 47	ся оз 0	n As	n Me	t Se	r Al 47	a G1 5	n Al	a Ly	ıs As	3n Trp 480
5	Le	eu Pr	o G1	y Pr	o Cy 48	s Ту 5	r Ar	g Gl	n Gl	n Ar 49	g Va O	l Se	r Th	r Th	r Le 49	u Ser 5
10	.g1	n Ası	n As:	n Ası 500	n Se. O	r As	n Pho	e Ala	a Try	p Thi	r Gl	y Al	a' Th	r Ly 51		r His
	Le	u Ası	51:	y Arc	J Ası	p Se:	r Lei	val 520	L Ası	n Pro	Gly	y Val	1 Ala 52		t Al	a Thr
15	Hi	s Lys 530	Asy )	qeA o	Gl:	ı GJ/	Arg 535	Phe	Phe	Pro	Ser	540		y Va	l Le	u Met
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	Trp	Gln 610	Asn	Arg	qeA	Val	Tyr 615	Leu	Gln	Gly	Pro	11e 620	Trp	Ala	Lys	Ile
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20						-						,				
25								•						,		
30																

	Met 1	: Ala	a Ala	Asp	61 y 5	Ty:	r Lei	ı Pro	e Ası	7 Tr 10	p Le	o Gl	u As <sub>l</sub>	neA q	Lei 15	u Ser
5	Glu	Gly	y Ile	Arg 20	Glu	Tr	Trp	eA o	Let 25	Ly:	Pro	, Gl	y Ala	a Pro	Lys	Pro
10	Lys	Ala	a Asņ 35	Gln	Gln	Lys	Glr	A 27 40	Asp	Gly	/ Arç	el?	/ Let 45	ı Val	. Lev	Pro
	Gly	Tyr 50	: Lys	Tyr	Leu	G7?	Pro 55	Phe	: Asn	Gly	Leu	Asp 60	Lys	Gly	Glu	Pro
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	Asp	Ala	Glu	Phe 100	Gln	Glu	Arg	Leu	Gln 105	Glu	Asp	Thr	Ser	Phe 110	Gly	Gly
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	Pro 145	Val	Glu	Pro	Ser	Pro 150	Gln	Arg	Ser	Pro	Asp 155	Ser	Ser	Thr	Gly	Ile 160
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	Pro 2	Ala	Gly :	Pro :	Ser (	Gly	Leu	Gly 200	Ser	Gly	Thr	Met	Ala 205	Ala (	ely	Gly

5	Gl	210 210		Met	: Ala	. Asp	215		Gl:	r ell	/ Ala	220		y Val	L Gly	/ Ser
	Ser 225		Gly	Asn	Trp	His 230		qeA	Ser	Thr	Trp 235		. Gly	Asp	Arg	Val 240
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15	Leu	Tyr	Lys	Gln 260		Ser	Asn	Gly	Thr 265		Gly	ely	Ser	Thr 270		qeA ı
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45	Pro	Ala	Asp	Pro 660	Pro	Thr	Thr	Phe	Ser 665	Gln	Ala	Lys	Leu	Ala 670	Ser	Phe
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	Gly	Thr	Tyr	Ser	Glu 725	Pro	Arg	Pro	Ile	Gly 730	Thr	Arg	Tyr	Leu	Thr 735	Arg
. 5																
	neA	Leu														
	,															
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10	Lys	Ala	Asn 35	Gln	Gln	Lys	Gln	, Asp 40	Asp	Gly	Arg	Gly	Leu 4,5	Val	Leu	Pro
	Gly	Tyr 50	Lys	Tyr	Leu	Gly	Pro 55	Phe	neA	Gly	Leu	Asp 60	Lys	Gly	Glu	Pro
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40	Pro	Ala	Gly 195	Pro :	Ser	Gly		Gly 200	Ser	Gly	Thr	Met	Ala 205	Ala	ely	Gly

5	Gly	/ Ala 210		Met	Ala	Asp	215		Glu	Gly	Ala	Asp 220	-	/ Val	. Gly	/ Ser
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		Le₁	l Pro	Gl;	Y Pro	485		: Arç	; Glr	Glr	490		l Ser	Thi	Thr	195	Ser
10		Glī	Asr	n Ası	500		: Asī	Phe	Àla	505		: Gl)	/ Ala	Thr	Lys 510		His
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		. His	Lys 530	qeA	qeA	Glu	Glu	Arg 535		Phe	Pro	Ser	Ser 540	Gly	Val	Leu	Met
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Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg 725 730 735

5																	
		Ası	a Lei	1													
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						, <sub>P</sub>	0, 0.0		•••								
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		Met 1	: Ala	Ala	Asp	Gly 5	Ty	Leu	Pro	qeA o	Trp 10	Lev	ı Glı	ı Ası	z Ası	Lev 15	Se
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		Glu	Gly	Ile	Arg 20	Glu	Trp	Trp	Ala	Leu 25	Lys	Pro	Gly	/ Ale	Pro 30	Lys	Pro
		Tara	715	7	c1-	~1 <u>~</u>	<b>7</b>	<b>~</b> 3	•								
25		гдз	WIG	35	GIN	GIN	гì	GIN	40	qeA o	GIA	' Arg	Gly	45	ı Val	. Leu	Pro
		Gly	Tyr 50	Lys	Tyr	Leu	Gly	Pro 55	Phe	neA	Gly	Leu	Asp 60	Lys	Gly	Glu	Pro
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		Asp	Ala	Glu ,	Phe 100	Gln	Glu	Arg	Leu	Gln 105	Glu	Ąsp	Thr	ser	Phe 110	еĵЪ	Gly
40			•						_								
	•	Asn	Leu	115	Arg	Ala	Val	Phe	Gln 120	Ala	Lys	Lys	Arg	Val 125	Leu	Glu	Pro
45		Leu	Gly 130	Leu	Val	Glu	Glu	Gly	Ala	Lys	Thr				Lys	Lys	Arg
			100					135					140				
	·	Pro 145	Val	Glu	Pro	Ser	Pro 150	Gln	Arg	Ser	Pro	Asp 155	Ser	Ser	Thr	Gly	Ile 160
50																	
	•	Gly	Lys	Lys	Gly	<b>Gln</b> 165	Gln	Pro	Ala		Lys 170	Arg	Leu	Asn	Phe	Gly 175	Gln
55		Thr	Gly	Asp	Ser 180	Glu	Ser	Val		Asp 185	Pro	Gln	Pro	Ile		Glu	Pro
										103					190		

	P;	ro A	la G	ly P 95	ro S	er G	ly L	eu G	ly s 00	er G	ly T	hr M	let.	Ala 205	Al.	a G	ly Gl
5	G	Ly A. 2:	la P: 10	ro M	et A	la A	sp A 2	sn A 15	sn G	lu G	ly A	la A 2	.sp :20	Gly	Va:	1 G1	y Sez
10	S e 2 2	er Se !5	er G	ly A:	sn Ti	rp H: 23	is C <sub>2</sub> 30	ys As	sp S	er T	hr T.	rp <sup>'</sup> L 35	eu (	Sly	Ası	G1	y Val 240
15	Il	e Th	ir Th	r Se	r Th	r Ar S	g Tì	ur Tr	p A	la L. 2!	eu P: 50	co T	hr 1	yr	Asn	<b>As</b> : <b>2</b> 5:	n His 5
15	Le	u Ty	r Ly	s G1 26	n Il 0	e Se	er As	n Gl	у Тì 26	nr Se 55	er Gl	.у G	ly s	er	Thr 270	Ası	n Asp
<b>20</b>	As	n Th	т Ту. 27.	r Ph 5	e Gl	у Ту	r Se	r Th 28	r Pr O	o Tr	p Gl	у Т		he . 85	Asp	₽h€	Asn
25	Ar	9 Pho 290	e Hi:	з - Су	s Hi	s Ph	e Se. 29	r Pro	Ar	g As	P Tr	p G]	Ln A	rg 1	Leu	Ile	ne <i>A</i> :
	Asr 305	Asr 5	ı Tr	Gl:	y Phe	310	g Pro	D Ly:	s Se	r Le	u As 31	n Ph 5	e L	ys I	ceu	Phe	Asn 320
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		. Se:	450	g Th. O	r Gl	n Se	r Th	r Gl 45		y Th	r Al	a Gl	y Th 46		n Gl	n Le	u Lei
5		Phe 465	e Sei	c Gl	n Al	a Gl	y Pr 47	о Аз 0	n As	n Me	t Se	r Al 47	a Gl 5	n Al	a Ly	s As:	n Tr 480
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		Glr	Asr	n Asr	Ası 500	n Se:	≿ Ası	n Ph	e Ala	9 Tr	p Thi	c Gly	y Ala	a Thi	Ly: 510		: His
15		Leu	. Asn	Gly 515	Arg	l Yai	Sei	. Lei	val 520	L Ası	n Pro	Gl;	/ Val	L Ala 525		: Ala	Thr
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22		Phe 545	Gly	Lys	Gln	Gly	7- Ala 550	Gly	' Lys	Asp	azA o	Val 555	Asp	Tyr	Ser	Ser	Val 560
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			.*														
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55			-														

5	Me 1	t Al	a Al	a Ası	5 G1	у Ту	r Le	u Pro	eA c	Tr; 10	) Let	ı Glu	ı As	eA q	n Le 15	u Ser
3	G1:	u Gl	y Il	e Arg 20	g Glu	ı Tr	p Tr	Asp	Lev 25	Ly:	Pro	Gly	/ Ala	30	b Ly	s Pro
10	Lys	Ala	Asr 35	ı Gln	Glr	Lys	G Glm	Asp 40	Азр	`Gly	' Arg	Gly	Let 45	l Val	L Le	u Pro
	Gly	Tyr 50	Lys	Tyr	Leu	Gly	Pro 55	Phe	neA	Gly	Leu	Asp 60	Lys	Gly	' Glu	Pro
15	Val 65	neA .	Ala	Ala	Asp	Ala 70	. Ala	Ala	Leu	Glu	His 75	Asp	Lys	Ala	Тух	45p
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	Pro 145	Val	Glu	Pro	Ser	Pro 150	Gln	Arg	Ser	Pro	Asp 155	Ser	Ser	Thr	Gly	Ile 160
35	Gly	Lys	Thr	ely	Gln 165	Gln	Pro .	Ala :	Lys :	Lys . 170	Arg :	Leu ;	Asn		Gly 175	Gln
40	Thr	Gly .	Asp	Ser ( 180	Glu	Ser '	Val :	Pro ;	Asp I	Pro (	5ln 1	Pro :		Gly 190	<b>Gl</b> u	Pro

	Pr	o Ala	19	y Pro	Se:	z Gly	y Let	200		r Gl	y Thi	r Met	20:		Gl;	y Gly '
5	Gl	y Ala 210	a Pro	o Met	Ala	a Asp	215		n Gli	u Gl	y Ala	220		y Val	l Gl	y Ser
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. 20	Asn	Thr	Tyr 275	Phe	Gly	Tyr	Ser	Thr 280		Trp	Gly	Tyr	Phe 285		Phe	Asn
	Arg	Phe 290	His	Cys	His	Phe	Ser 295	Pro	Arg	qeA	Trp	Gln 300	Arg	Leu	Ile	neA
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40	Pro	Ala 370	ĄSĄ	Val	Phe	Met	Ile 375	Pro	Gln	Tyr	Gly	Tyr 380	Leu	Thr	Leu	Asn
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ı	Leu		Arg 435	Leu :	Met	Asn		Leu 440	Ile	qeA	Gln '		Leu 445	Tyr	Tyr	Leu

		Sei	450	Thi	r Gli	n Se	r Th.	45	y G1: 5	y Th	r Ale	a Gl	y Th 46		n Gl	n Lei	ı Let
5		Phe 465	e Ser	Gl:	a Ala	a G1;	y Pr 470	0 A31	n Ası	n Me	t Se	47	a Gl	n Al	a Ly	s Ası	480
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20		His	Lys 530	Ąsp	qeA	Glu	Glu	Arg 535		Phe	Pro	Ser	Ser 540		Val	Leu	Met
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10		Gl	y Ala 210	a Pro	Met	: Ala	e As	215	n Ası 5	n Gl	u Gl	y Al	a As 22		y Vai	, GI	y Ser
15		Se: 225	r Ser	: Gly	Asr	ı Trp	230	Cys	a Asp	Sei	Th:	Tr 235		n ej	qeA v	Arg	y Val 240
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25			His	Lys 530	Ąap	Asp	Glu	Glu	Arg 535	Phe	Phe	Pro	Ser	Ser 540	Gly	Val	Leu	Met
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	Hi: 22	s Cy:	zeA e	Ser	Thr	Trp 230	) Lev	ı Gly	y As <sub>i</sub>	Arq	7 Val 235		th:	Thr	: Se:	Thr 240
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Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys 690 695 700

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55												•					

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	Ası	210	n Asn	Gl:	1 Gly	y Ala	Asp 215		y Val	l Gl	y Sea	22		r Gl	y Ası	n Trp
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_	9 7	er Th 05	r Ası	n Val	. Asp	710	Ala )	Val	reA l	r Thi	.715		y Thi	ту	Se:	720
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		G1	y Le	u Gl 19	y Se S	r Gl	y Th	ır Me	t Al 20		La G	ry Gl	y G1	.γ Α] 20		o Me	et Ala
5	·	As	p As 21	n As 0	n Gl	u Gl	y Al	a As 21	p G1 5	y Va	1 61	y As	n Al 22		r Gl	y As	n Trp
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	Asr 465	Met	; șe:	: Ala	Glz	1 Ala 470		Asn	Trp	Lev	475		Pro	Cys	з Ту	480
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		Hi: 225	s Cys	geA s	Ser	Thi	230		ı Gly	/ Ası	Arg	Val 235		Thi	Thi	: Sei	7hr 240
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55																	

			Tyr	Arg	Gln	Gln	Arg 485		. Ser	Thr	Thr	Val 490		Gln	ı Asn	Asn	Asn 495	Ser
5			Asn	Phe	Ala	Trp 500		Gly	Ala	Thr	Lys 505		His	Leu	Asn	Gly 510		qеA
10		•	Ser	Leu	Val 515		Pro	Gly	Val	Ala 520		Ala	Thr	His	Lys 525		Asp	Glu
45			Glu	Arg 530		Phe	Pro	ser	Ser 535		Val	Leu	Met	Phe 540	СŢУ	Lys	Gln	GJ <b>Ā</b>
15			Ala 545		Lys	Asp	Asn	Val 550	Asp	Tyr	Ser	Ser	Val 555	Met	Leu	Thr	Ser	Gl <u>u</u> 5 <b>60</b>
20	~		Glu	Glu	Ile	Lys	Thr 565	Thr	Asn	Pro	Val	Ala 570	Thr	Glu	Gln	Tyr	Gly 575	Val
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25			Val	Asn	ser 595	Gln	Gly	Ala	Leu	Pro 600	Gly	Met	Val	Trp	Gln 605	Asn	Arg	Asp
30			Val	Tyr 610	Leu	Gln	Gly	Pro	Ile 615	Trp	Ala	Lys	Ile	Pro 620	His	Thr	Asp	eĵÀ
35			Asn 625	Phe	His	Pro	Ser	Pro 630	Leu	Met	Gly	Gly	Phe 635	Gly	Leu	Lys	His	Pro 640
33			Pro	Pro	Gln	Ile	Leu 645	Ile	Lys	Asn	Thr	Pro 650	Val	Pro	Ala	Asp	Pro 655	Pro
40			Thr	Thr	Phe	Ser 660	Gln	Ala	Lys	Leu	Ala 665	Ser	Phe	Ile	Thr	Gln 670	Tyr	Ser
45			Thr	Gly	Gln 675	Val	Ser	Val	Glu	Ile 680	Glu	Trp	Glu	Leu	Gln 685	Lys	Glu	<b>A</b> S <b>N</b>
45			Ser	Lys 690	Arg	Trp	Asn	Pro	Glu 695	Ile	Gln	Tyr	Thr	Ser 700	Asn	Tyr	Tyr	Lys
50			Ser 705	Thr	Asn	Val		Phe 710	Ala	Val	Asn	Thr	Glu 715	Gly	Thr	Tyr		Glu 720
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10		Gli	u Gly	y Ile	Arg 20	g Gli	Tr	o Trp	eA c	p Le 25	u Ly:	s Pro	o Gly	/ Ala	9 Pro	Ly.	s Pro
		Lys	. Ala	35	Gln	Gln	Lys	Glr.	Asp 40	e As	p Gly	/ Arq	g Gly	/ Let 45	ı Val	Let	ı Pro
15		GJ7	7 Tyr 50	Lys	Tyr	Leu	Gly	7 Pro	Phe	e Ası	r ell	Let	Asp 60	Lys	Gly	Gl:	Pro
		Val 65	. Asr	Glu	Ala	qeA	Ala 70	Ala	Ala	Lei	ı Glu	His 75	Asp	Lys	Ala	Туг	q <b>z</b> A :
20		Lys	Gln	Leu	Glu	Gln 85	Сĵ	Asp	Asn	Pro	90	Leu	Lys	Tyr	Asn	His 95	Ala
25		Asp	Ala	Glu	Phe 100	èju	Glu	Arg	Leu	Gln 105	Glu	Asp	Thr	Ser	Phe 110	Gly	Gly
		neA	Leu	Gly 115	Arg	Ala	Val	Phe	Gln 120	Ala	Lys	Lys	Arg	Val 125	Leu	Glu	Pro
30		Leu	Gly 130	Leu	Val	Glu	Glu	Gly 135	Ala	Lys	Thr	Ala	Pro 140	Gly	Lys	Lys	Arg
35		Pro 145	Val	Glu	Pro	ser	Pro 150	Gln	Arg	Ser	Pro	Asp 155	Ser	Ser	Thr	Gly	Ile 160
40		ely	Lys	Thr	Gly	Gln 165	Gln	Pro	Ala	Lys	Lys 170	Arg	Leu	Asn	Phe	Gly 175	Gln
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45		Pro	Ala	Gly 195	Pro	Ser	Gly	Leu	Gly 200	Ser	Gly	Thr		Ala 205	Ala	ета	Gly
		Gly	Ala 210	Pro :	Met .	Ala .	Asp	Asn 215	Asn	Glu	Сĵу		Asp 220	Gly	Val	Gly	Ser
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55		Ile	Thr	Thr :	Ser '	Thr 1 245	Arg	Thr '	Trp		Leu 250	Pro	Thr '	Tyr		Asn 255	His

	Le	u Ty	r Ly	260	n Il O	e Se	e.A. z	n Gl	y Th: 26:		r Gly	y Gl	y Se.	270		qeA n
5	еA	n Th	275	r Phe	e Gl	y <b>Ty</b> :	r Sei	Th: 280		Tr	el?	ү Ту.	r Phe 28		Phe	aeA e
10	Ar	g Pho 290	e His	в Суз	Hi:	s Phe	295		Ar	g Asp	Trp	300		, Leu	ı Ile	neA :
	As:	n Asr 5	Trp	Gly	/ Phe	310		Lys	Arg	, Leu	Asn 315		e Lys	Lev	Phe	Asn 320
15	IĻ	e Glr	Val	Lya	G1v 325	ı Val	Thr	Gln	. Asn	330	ely	Thi	Lys	Thr	11e 335	
20	Ası	Asn	Leu	Thr 340	Ser	Thr	Ile	Gln	Val 345		Thr	Asp ,	) Ser	Glu 350		Gln
	Lev	Pro	Tyr 355	Val	Leu	Gly	Ser	Ala 360	His	Gln	Gly	Суз	Leu 365		Pro	Phe
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	 Gln	Asn	Asn	Asn 500	Ser	Asn	Phe		Trp 505	Thr	Gly .	Ala	Thr	Lys 510	Tyr	His

		Le	u Ası	n Gly 515	/ Arg	g Asp	Se.	r Lei	1 Va: 520		n Pro	o Gly	y Va:	1 Al. 52		t Al	a Thr
5		Hi	5 Lys	a Asp	Asp	Glu	Gl:	1 Arg 535		Phe	e Pro	Se:	540		y Val	l Lei	ı Met
10		Phe 545	e Gly	, Lys	Glm	Gly	Ala 550	a Gly	' Lys	Asp	Asn	Val 555		ту:	: Se	: Se	Val 560
		Met	Leu	Thr	Ser	Glu 565	Gli	Glu	Ile	Lys	Thr 570		Asn	Pro	Val	Ala 575	Thr
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		Тгр	Gln 610	Asn	Arg	Asp	Val	Туг 615	Leu	Gln	Gly	Pro	Ile 620	Trp	Ala	Lys	Ile
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		Pro	Ala	Asp	Pro 660	Pro	Thr	Thr	Phe	Ser 665	Gln	Ala	Lys	Leu	Ala 670	Ser	Phe
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		ser 705	Asn	Tyr	Tyr	Lys	<b>Ser</b> 710	Thr	Asn	Val		Phe 715	Ala	Val	Asn	Thr	Glu 720
45		Gly	Thr	Tyr	Ser	Glu 725	Pro	Arg	Pro	Ile	Gly '	Thr .	Arg	Tyr	Leu	Thr 735	Arg
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55	<213> ca		rotein	of AA\	V serc	type,	cione	43.1									

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10   Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro   50   S5   Phe Asn Gly Leu Asp Lys Gly Glu Pro   65   Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp   65   Asn Ala Ala Asp Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala   85   85   85   85   85   85   85   8	5		Glu	Gly	Ile		Glu	Trp	Trp	qeA ·		Lys	Pro	Gly	Ala		Lys	Pro
50 55 60  15 Val Asn Ala Ala Asp Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Ass Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala 20  Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly 100  Asp Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro 115  Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg 130  Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile 145  Gly Lys Lys Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln 175  Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro 185  Fro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly 195  Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 225  Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val 240  Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His	10		Lys	Ala		Gln	Gln	Lys	Gln		Asp	Gly	Arg	Gly		Val	Leu	Pro
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala 85 Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly 100 asp Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro 125 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg 130 asp Thr Ser Thr Gly Ile 150 asp Thr Ala Pro Gly Lys Lys Arg 130 asp Thr Ala Pro Gly Lys Lys Arg 130 asp Thr Ala Pro Gly Lys Lys Arg 130 asp Thr Ala Pro Gly Lys Lys Arg 130 asp Thr Ala Pro Gly Lys Lys Arg 130 asp Thr Ala Arg Lys Arg 140 asp Ser Ser Thr Gly Ile 150 asp Tro Ala Arg Lys Arg Leu Asn Phe Gly Gln 165 asp Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro 180 asp 180 asp Tro Ala Arg Lys Arg Leu Asn Phe Gly Glu Pro 180 asp 180 asp Tro Ala Arg Lys Arg Leu Asp Gly Gly Gly 195 asp Ser Gly Ala Asp Gly Gly Val Gly Ser Gly Ala Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly 200 asp Ser Ser Thr Trp Leu Gly Asp Arg Val 225 asp Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val 195 asp Ser Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His			Gly	50	Lys	Tyr	Leu	Gly		Phe	Asn	Gly	Leu		Lys	eĵà	Glu	Pro
20  Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly 100	15			Asn	Ala	Ala	- Asp		Ala	Ala	Leu	Glu		Ąsp	Lys	Ala	Tyr	
25 Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro 115 Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg 130 Pro Val Glu Pro 125 Ser Pro Asp Ser Pro Asp Ser Ser Thr Gly Ile 145 Gly Lys Lys Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Pro 165 Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro 185 Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro 185 Gly Asp Ser Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly 195 Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val 225 Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His	. 20		Gln	Gln	Leu	Lys		Gly	Asp	Asn	Pro		Leu	Arg	Tyr	Asn		Ala
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg 130  Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile 145  Gly Lys Lys Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln 165  Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro 180  Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly 195  Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 210  Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val 225  Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His			Asp	Ala	Glu	Phe 100	Gln	Glu	Arg	Leu		Glu	Asp	Thr	Ser		Gly	Gly
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile 145    Gly Lys Lys Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln 165    Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro 185    Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly 195    Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val 225    Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His	25		neA	Leu		Arg	Ala	Val	Phe		Ala	Lys	Lys	Arg		Leu	Glu	Pro
Gly Lys Lys Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln 165  Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro 180  Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly 195  Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val 225  Tle Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His	30		Leu		Leu	Val	Glu	Glu		Ala	ГÀЗ	Thr	Ala		Gly	Lys	Lys	Arg
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro 180  Fro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly 205  Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 215  Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val 225  Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His				Val	Glu	Pro	Ser		Gln	Arg	Ser	Pro		9er	Ser	Thr	Gly	
Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly 195  Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser 215  Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val 220  Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His	35		Gly	Lys	Lys	Gly		Gln	Pro	Ala	Arg		Arg	Leu	Asn	Phe		Gln
Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val 225  195  195  200  205  205  207  208  208  209  209  207  208  208  209  209  209  209  200  200	40		Thr	Gly	Asp		Glu	Ser	Val	Pro		Pro	Gln	Pro	Ile		Glu	Pro
Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val 225 230 235 240  Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His			Pro	Ala		Pro	Ser	Gly	Leu		Ser	Gly	Thr	Met		Ala	Gly	Сĵ
225 230 235 240 50  Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His	45		Gly		Pro	Met	Ala	qeA		Asn	Glu	Gly	Ala		Gly	Val	ely	Ser
	50 .			Ser	Gly	Asn			Cys	Asp .	Ser	Thr		Leu	ely	qeA	Arg	
		•	Ile	Thr	Thr	Ser		Arg	Thr	Trp	Ala		Pro	Thr	Tyr	Asn		His

5		Le	u Ty	r Ly	s Gl 26	n Il O	e Se	r As	n Gl	y Th 26		r Gl	y Gl	y Se	r Th 27		qeA n
		Ası	n Th	r Ty 27	r Ph	e Gl	у Ту:	r Se	r Th: 28	r Pr O	o Tr	p Gl	у Ту	r Ph 28		p Ph	e Asn
10		Ar	290	e Hi	s Cy:	s Hi	s Pho	e Se: 29:	r Pro	o Ar	g As	p Tr	30		g Le	u Il	e Asn
		Asr 305	Ası	Tr	p Gly	y Pho	310	g Pro	Lys	Ar	g Lei	1 Asr 315		≥ Ly:	s Le	ı Phe	320
15		Ile	: Glr	Val	L Lys	325	ı Val	Thi	Glr	a Ası	330		Thi	Ly:	3 Thi	: Ile 335	Ala
20		neA	Asn	Leu	340	Ser	Thr	: Ile	Gln	Va] 345	Phe	: The	'Asr	Sez	350		Gln
		Leu	Pro	Tyr 355	Val	Pro	Gly	'Ser	Ala 360	His	Gln	Gly	Суз	Leu 365		Pro	Phe
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		Ser	Arg 450	Thr	Gln	Ser	Thr	Gly 455	Gly			Gly			Gln	Leu	Leu
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50						485					490					Leu 495	
	ì	Gln .	Asn	neA	<b>Asn</b> 500	Ser	Asn	Phe		Trp 505	Thr	Gly	Ala	Thr	Lys 510	Tyr	His
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		His	Lys 530		Asp	Glu	Glu	Arg 535	Phe	Phe	Pro	Ser	Ser 540		Val	Lev	Met
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10		Met	Ļeu	Thr	Ser	Glu 565	Glu	Glu	Ile	Lys	Thr 570	Thr	Asn	Pro	Val	Ala 575	,Thr
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25		Gly	Leu	Lys	His	Pro 645	Pro	Pro	Gln	Ile	Leu 650	Val	Lys	Asn	Thr	Pro 655	Val
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		Leu	Gln 690	Lys	Glu	neA	Ser	Lys 695	Arg	Trp	Asn	Pro'	Glu 700	Ile	Gln	Tyr	Thr
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		Asn	Leu														
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55	<400> 9			- •		, F =1.	,										

		Me 1	t Al	a Al	a Ası	p Gl 5	у Ту	r Le	u Pr	c As	p Tr 10	p Le	u Gl	u As	p As	n Le	u Se
5		Gl	u Gl	y Il	e Arg 20	g Gl	u Tr	p Tr	lsy d	25	u Ly	s Pr	o G1	y Al	a Pr 30	o Ly	9 Pro
10		Ly	s Ala	8 Ası 35	n Glm	Gl:	n Ly:	s Gl	n Asy 40	As <sub>1</sub>	p Gl	, Y Ar	g Gl	y Let 45	ı Va	l Le	ı Pro
		G1;	у Ту: 50	t Lys	3 Tyr	Leu	ı Gly	7 Pro	Phe	e Ası	n Gly	y Lei	1 As <sub>1</sub> 60	p Lys	G G1	y Gli	Pro
15		Va: 65	l Asr	a Ala	Ala	ze.	70	Ala	a Ala	Let	ı Glü	His 75	3 Ası	D Lys	Ala	а Туг	qeA : 08
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		Asp	Ala	Glu	Phe 100	Gln	Glu	Arg	Leu	Gln 105	Glu	. Asp	Thr	Ser		e Gly	Gly
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		Pro 145	Val	Glu	Pro	Ser	Pro 150	Gln	Arg	Ser	Pro	Asp 155	Ser	Ser	Thr	Gly	Ile 160
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		Pro	Ala	Gly 195	Pro	Ser	Gly	Leu	Gly 200	Ser	Gly	Thr	Met	Ala 205	Ala	Gly	Gly
45	·	Gly	Ala 210	Pro	Met i	Ala	qeA	Asn 215	Asn	Glu	ely		Asp 220	Gly	Val	Gly	Ser
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	ı	Ile	Thr	Thr	Ser 1	Thr . 245	Arg '	Thr	Trp 2		Leu 250	Pro	Thr	Tyr :		Asn : 255	His

		Leu	Tyr	Lys	Gln 260		. Ser	. Asn	Gly	265		: Gly	Gly	sez	270		qeA ı
5		Asn	Thr	Tyr 275		Gly	Tyr	: Ser	Thr 280		Trp	Gly	Туг	Phe 285	_	Phe	: Asn
10		Arg	Phe 290		eyo	His	Phe	Ser 295		Arg	Asp	Trp	Gln 300	_	Leu	Ile	Asn
		Asn 305		Trp	Gly	Phe	Arg 310		Lys	Arg	Leu	Asn 315	Phe	Lys	Leu	Phe	Asn 320
15		Île	Gln	Val	Lys	Glu 325	Val	Thr	Gln	Asn	330 GJ <i>n</i>	Gly	Thr	Lys	Thr	Ile 335	Ala
20		Asn	neA	Leu	Thr 340	Ser	Thr	Ile	Gln	Val 345		Thr	Asp	Ser	Glu 350	Tyr	Gln
		Leu	Pro	Tyr 355	Val	Leu	GJĀ	Ser	Ala 360	His	Gln	Gly	Суз	Leu 365	Pro	Pro	Phe
25		Pro	Ala 370	Asp	Val	Phe	Met	Ile 375	Pro	Gln	Tyr	Gly	Tyr 380	Leu	Thr	Leu	Asn
30	٠	Asn 385	Gly	Ser	Gln	Ala	Val 390	Gly	Arg	Ser	Ser	Phe 395	Tyr	Cys 、	Leu	Glu	Tyr 400
		Phe	Pro	Ser	Gln	Met 405	Leu	Arg	Thr	Gly	Asn 410	Asn	Phe	Glu	Phe	Ser 415	Tyr
35		Thr	Phe	Glu	Asp 420	Val	Pro	Phe	His	Ser 425	Ser	Tyr	Ala	His	Ser 430	Gln	Ser
40		Leu	Asp	Arg 435	Leu	Met	Asn	Pro	Leu 440	Ile	Asp	Gln	Tyr	Leu <sup>.</sup> 445	Tyr	Tyr	Leu
		Ser	Arg 450	Thr	Gln	Ser	Thr	Gly 455	Gly	Thr	Gln	Gly	Thr 460	Gln	Gln	Leu	Leu
45		Phe 465	Ser	Gln	Ala	Gly	Pro 470	Ala	Asn	Met	Ser	Ala 475	Gln	Ala	Lys	Asn	Trp 480
50		Leu	Pro	Gly	Pro	Cys 485	Tyr	Arg	Gln	Gln	Arg 490	Val	Ser	Thr	Thr	Leu 495	Ser
	·	Gln	Asn	Asn	Asn 500	Ser	neA	Phe	Ala	Trp 505	Thr	Gly	Ala	Thr	Lys 510	Tyr	His
55																	

		Lev	ı Asr	515		g Asp	Sei	: Leu	520		Pro	, el	Val	525		: Ala	Thr
5		His	530		qeA o	Glu	Gli	Arg 535		Phe	Pro	Ser	Ser 540		Val	Leu	1 Met
10		Phe 545		. Lys	Gln	Gly	Ala 550		Lys	Asp	Asn	Val 555		Tyr	Ser	: Ser	Val 560
		Met	Leu	Thr	Ser	Glu 565	Glu	Glu	Ile	Lys	Thr 570	Thr	Asn	Pro	Val	Ala 575	Thr
15		Glu	Gln	Tyr	Gly 580	Val	Val	Ala	Asp	Asn 585	Leu	Gln	Gln	Thr	Asn 590		Ala
20		Pro	Ile	Val 595	Gly	Thr	Val	Asn	Şer 600	Gln	Gly	Ala	Leu	Pro 605	Gly	Met	Val
		Trp	Gln 610	neA	Arg	Asp	Val	Tyr 615	Lau	Gln	Gly	Pro	Ile 620	Trp	Ala	Lys	Ile
25		Pro 625	His	Thr	qeA	Gly	Asn 630	Phe	His	Pro	Ser	Pro 635	Leu	Met	Gly	Gly	Phe 640
30		Gly	Leu	Lys	His	Pro 645	Pro	Pro	Gln	Ile	Leu 650	Val	Lys	Asn	Thr	Pro 655	Val
o.c		Pro	Ala	Asp	Pro 660	Pro	Thr	Thr	Phe	Ser 665	Gln	Ala	Lys	Leu	Ala 670	Ser	Phe
35		Ile	Thr	Gln 675	Tyr	Ser	Thr	Gly	Gln 680	Val	Ser	Val	Glu	Ile 685	Glu	Trp	Glu
40		Leu	Gln 690	Lys	Glu	Asn	Ser	Lys 695	Arg	Trp	Asn		Glu 700	Ile	Gln	Tyr	Thr
		Ser 705	Asn	Tyr	Tyr	Lys	Ser 710	Thr	Asn	Val	Asp	Phe 715	Ala	Val	Asn	Thr	Glu 720
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	<400> 94	osiu pi	oteni (	ai run V	3610	ıyp <del>e</del> , (	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	-0.0									

	Me: 1	E Ala	Ala	a Asp	5 5	Ty	r Leu	Pro	Asp	Trp 10	Lev	Gl:	ı Asp	Asr	Lei 15	ı Ser
5	Gli	. G]}	/ Ile	Arg 20	Glu	Tr	Trp	geA o	25	Lys	Pro	Gl)	/ Ala	Pro 30	Lys	Pro
10	Lys	Ala	Asn 35	Gln	Gln	Lys	Gln	Asp 40	Asp	Gly	Arg	Gly	/ Leu 45	Val	. Leu	Pro
	Gly	Tyr 50	: Lys	Tyr	Leu	Gly	Pro 55	Phe	Asn	Gly	Leu	Asp 60	Lys	Gly	Glu	Pro
15	Val 65	. Asn	Ala	Ala	Asp	Ala 70	Ala	Ala	Leu	Glu	His 75	Asp	Ļys	Ala	Tyr	qeA 08
20	Gln	Gln	Leu	Lys	Ala 85	Gly	Asp	Asn	Pro	Tyr 90	Leu	Arg	Tyr	Asn	His 95	Ala
	Asp	Ala	Glu	Phe 100	Gln	Glu	Arg	Leu	Gln 105	Glu	qeA	Thr	Ser	Phe 110	ely	Gly
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30	Leu	Gly 130	Leu	Val	Glu	Glu	Gly 135	Ala	Lys	Thr	Ala	Pro 140	Gly	Lуз	Lys	Arg
	Pro 145	Val	Glu	Pro	Ser	Pro 150	Gln	Arg	Ser	Pro	Asp 155	Ser	Ser	Thr	Gly	Ile 160
	Gly	'Lys	Lys	GJA	His 165	Gln	Pro	Ala	Arg	Lys 170	Arg	Leu	Asn	Phe	Gly 175	Gln
40	Thr	Gly	qeA	Ser 180	Glu	Ser	Val	Pro	Asp 185	Pro	Gln	Pro	Ile	Gly 190	Glu	Pro
	Pro	Ala	Gly 195	Pro	Ser	<u>e</u> ly	Leu	Gly 200	Ser	Gly	Thr	Met	Ala 205	Ala <sub>.</sub>	Gly	Gly
		210					215					220			Gly	
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	Ile	Thr	Thr	Ser	Thr 245	Arg	Thr	Trp		Leu 250	Pro '	Thr	Tyr		Asn 255	His

			Leu	Tyr	Lys	Gln 260		. Ser	Asn	Gly	Thr 265		Gly	Gly	Ser	Thr 270		qeA
5			Asn	Thr	Tyr 275		Gly	Tyr	Ser	Thr 280		Trp	Gly	Tyr	Phe 285		Phe	Asn
10			Arg	Phe 290		Суз	His	Phe	Ser 295		Arg	qeA	Trp	Gln 300	Arg	Leu	Ile,	neA ,
			Asn 305		Trp	Gly	Phe	Arg 310		Lys	Arg	Leu	Asn 315		Lys	Leu	Phe	Asn 320
15			Ile	Gln	Val	Lys	Glu 325		Thr	Gln	Asn	330 GJ <i>n</i>	Gly	Thr	Lys	Thr	Ile 335	Ala
20			· Asn	· Asn	Leu	Thr 340	Ser	Thr	Ile	Gln	Val 345		Thr	Asp	Ser	Glu 350	Tyr	Gln
25			Leu	Pro	Tyr 355	Val	Leu	Gly	Ser	Ala 360	His	Gln	Gly	Cys	Leu 365	Pro	Pro	Phe
25	-	•	Pro	Ala 370	qeA	Val	Phe	Met	Ile 375	Pro	Gln	Tyr	Gly	Tyr 380	Leu	Thr	Leu	Asn
30			Asn 385	Gly	Ser	Gln	Ala	Val 390	Gly	Arg	Ser	Ser	Phe 395	Tyr	Суз	Leu	Glu	Tyr 400
35			Phe	Pro	Ser	Gln	Met 405	Leu	Arg	Thr	Gly	Asn 410	Asn	Phe	Glu	Phe	Ser 415	Tyr
			Thr	Phe	Glu	Asp 420	Val	Pro	Phe	His	Ser 425	Ser	Tyr	Ala	His	Ser 430	Gln	Ser
40			Leu	Asp	Arg 435	Leu	Met	Asn	Pro	Leu 440	Ile	Ąsp	Gln	Tyr	Leu 445	Tyr	Tyr	Leu
45			Ser	Arg 450	Thr	Gln	Ser	Thr	Gly 455	Gly	Thr	Gln	Gly	Thr 460	Gln	Gln	Leu	Leu
			Phe 465	Ser	Gln	Ala	Gly	Pro 470	Ala	neA	Met	Ser	Ala 475	Gln	Ala	Lys	neA	Trp 480
50	,		Leu	Pro	Gly	Pro	Cys 485	Tyr	Arg	Gln	Gln	Arg 490	Val	Ser	Thr	Thr	Leu 495	Ser
55			Gln	aeA	neA	neA 000	Ser	Asn	Phe	Ala	Trp 505	Thr	Gly	Ala	Thr	Lys 510	Tyr	His

	Lev	ı Asn	515	-	Asp	Ser	Leu	520		Pro	GIÀ	Val	525		AIB	Thr
5	His	Lys 530	•	Asp	Glu	Glu ·	Arg 535	Phe	Phe	Pro	Ser	Ser 540	_	Val	Leu	Met
10	Phe 545		Lys	Ģln	Gly	Ala 550	Gly	Lys	Asp	Asn	Val 555		Tyr	Ser	Ser	Val 560
15	Met	Leu	Thr	Ser	565	Glu	Glu	Ile	Lys	Thr 570	Thr	Asn	Pro	Val	Ala 575	Thr
13	Glu	Gln	Tyr	Gly 580	Val	Val	Ala	Asp	Asn 585	Leu	Gln	Gln	Thr	neA 590	Gly	Ala
20	Pro	Ile	Val 595	Gly	Thr	Val	Asn	Ser 600	Gln	GŢĀ	Ala	Leu	Pro 605	ely	Met	Val
25	Trp	Gln 610	Asn	Arg	Asp	Val	Tyr 615	Leu	Gln	Gly	Pro	Ile 620	Trp	Ala	Lys	Ile
	Pro 625			qeA	Gly	Asn 630	Phe	His	Pro	Ser	Pro 635	Leu	Met	GŢÀ	Gly	Phe 640
30	Gly	Leu	Lys	His	Pro 645	Pro	Pro	Gln	Ile	Leu 650	Val	Lys	Asn	Thr	Pro	Val
35	Pro	Ala	Asp	Pro 660	Pro	Thr	Thr	Phe	Ser 665	Gln.	Ala	Lys	Leu	Ala 670	Ser	Phe
	Ile	Thr	Gln 675	Tyr	Ser	Thr	Gly	680	Val	Ser	Val	Glu	Ile 685	Glu	Trp	Glu
40	Leu	Gln 690	Lys	Glu	aeA	Ser	Lys 695	Arg	Trp	Asn	Pro	Glu 700	Ile	Gln	Tyr	Thr
45	Ser 705	neA	Tyr	Tyr	Lys	ser 710	Thr	Asn	Val	qeA	Phe 715	Ala	Val	Asn	Thr	Glu 720
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	<210> 95															
,	<211> 738															
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<213> capsid protein of AAV serotype, clone AAV8

<400> 95

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5	Glu	Gly	, Ile	Arg 20	Glu	Tx;	Tr	Ala	Let 25	ı Lys	Pro	el?	Ala	Pro 30	Lys	Pro
10	Lys	Ala	35	Gln	Gln	Lys	Gln	40	Asp	GJY	/ Arg	. ej?	45	Val	Leu	Pro
	. ely	Tyr 50	Lys	Tyr	Leu	. Gly	Pro 55	Phe	ne.A	ejy	Leu	Asp 60	Lys	Gly	Glu	Pro
15	Val 65	Asn	Ala	Ala	'Asp	Ala 70	Ala	Ala	Leu	Glu	His 75	Asp	Lys	Ala	Tyr	Asp 80
20				Gln	85					90					95	
25				Phe 100					105					110		_
25			115	Arg				120					125			
30		130		Val			135					140				
35	145			Pro		150					155					160
					165					170					175	
40				Ser 180					185					190		
<b>45</b>			132	Pro				200					205			
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50	Ser 225	ser	GTŸ.	Asn !	rrp :	His 230	Суз .	Asp	Ser '		Trp 235	Leu	Gly .	Asp :		Val 240

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10		Asn	Thr	Tyr 275		Gly	Tyr	Ser	Thr 280		Trp	Gly	Tyr	Phe 285	_	Phe	Asn
15		Arg	Phe 290		Суз	His	Phe	Ser 295		Arg	qeA	Trp	Gln 300	_	Leu	Ile	Asn
		Asn 305		Trp	ely	Phe	Arg 310		Lys	Arg	Leu	Ser 315		Lys	Leu	Phe	Asn 320
20		Ile	Gln	Val	Lys	Glu 325		Thr	Gln	Asn	Glu 330		Thr	Lys	Thr	Ile 335	Ala
25		Asn	. Asn	Leu	Thr 340	Ser	Thr	Ile	Gln	Val 345	Phe	Thr	Asp	Ser	Glu 350	Tyr	Gln
		Leu	Pro	Tyr 355	Val	Leu	Gly	Ser	Ala 360	His	Gln	Gly	Суз	Leu 365	Pro	Pro	Phe
30		Pro	Ala 370	Asp	Val	Phe	Met	Ile 375	Pro	Gln	Tyr	Gly	Tyr 380	Leu	Thr	Leu	aeA
35		Asn 385	Gly	Ser	Gln	Ala	Val 390	Gly	Arg	Ser	Ser	Phe 395	Tyr	Cys	Leu	Glu	Tyr 400
		Phe	Pro	Ser	Gln	Met 405	Leu	Arg	Thr	Gly	Asn 410	Asn	Phe	Gln	Phe	Thr 415	Tyr
40		Thr	Phe	Glu	Asp 420	Val	Pro	Phe	His	Ser 425	Ser	Tyr	Ala	His	Ser 430	Gln	Ser
45		Leu	Asp	Arg 435	Leu	Met	Asn	Pro	Leu 440	Ile	qzA	Gln	Tyr	Leu 445	Tyr	Tyr	Leu
		Ser	Arg 450	Thr	Gln	Thr	Thr	Gly 455	Gly	Thr	Ala	Asn	Thr 460	Gln	Thr	Leu	Gly
50	,	Phe 465	Ser	Gln	Gly	Gly	Pro 470	neA	Thr	Met	Ala	Asn 475	Gln	Ala	Lys	Asn	Trp 480
<i>55</i>		Leu	Pro	Gly	Pro	Cys 485	Tyr	Arg	Gln	Gln	Arg 490	Val	Ser	Thr	Thr	Thr 495	Gly

	Gln	Asn	Asn	Asn 500	Ser	neA	Phe	Ala	Trp 505		Ala	Gly	Thr	Lys 510		His
5	Leu	Asn	Gly 515		Asn	Ser	Leu	Ala 520	Asn	Pro	Gly	Ile	Ala 525		Ala	Thr
10	His	Lys 530		Asp	Glu	Glu	Arg 535		· Phe	Pro	Ser	Asn 540		Ile	Leu	Ile
	Phe 545	Gly	Lys	Gln	Asn	Ala 550		Arg	qeA	Asn	Ala 555	qeA	Týr	Ser	Asp	Val 560
15	Met	Leu	Thr	Ser	Glu 565	Glu	Glu	Ile	Lys	Thr 570	Thr	Asn	Pro	Val	Ala 575	
20	Glu 	Glu	Tyr	Gly 580	Ile	Val	Ala	qeA	Asn 585	Leu	Gln	Gln	Gln	Asn 590	Thr	Ala
25	Pro	Gln	Ile 595	СŢĀ	Thr	Val	Asn	Ser 600	Gln	Gly	Ala	Leu	Pro 605	Gly	Met	Val
	Trp	Gln 610		Arg	Asp	Val	Tyr 615	Leu	Gln	Gly	Pro	Ile 620	Trp	Ala	Lys	Ile
30	Pro 625	His	Thr	Asp	Gly	Asn 630	Phe	His	Pro	Ser	Pro 635	Leu	Met	Gly	Gly	Phe 640
35	GŢĀ	Leu	Lys	His	Pro 645	Pro	Pro	Gln	Ile	Leu 650	Ile	Lys	Asn	Thr	Pro 655	Val
33	Pro.	Ala	Asp	Pro 660	Pro	Thr	Thr	Phe	Asn 665	Gln	Ser	Lys	Leu	Asn 670	Ser	Phe
40	Ile	Thr	Gln 675	Tyr	Ser	Thr	Gly	Gln 680	Val	Ser	Val	Glu	Ile 685	Glu	Trp	Glu
45	Leu	Gln 690	Lys	Glu	neA	Ser	Lys 695	Arg	Trp	Asn	Pro	<b>Glu</b> 700	Ile	Gln	Tyr	The
	Ser 705	Asn	Tyr	Tyr	Lys	Ser 710	Thr	Ser	Val	Asp	Phe 715	Ala	Val	Asn	Thr	Glu 720
50	elà	Val	Tyr		Glu 725	Pro	Arg	Pro		Gly 730	Thr	Arg	Tyr	Leu	Thr 735	Arg
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<210> 96 <211> 736

<212> PRT	
<213> capsid protein of AAV serotype, c	lone 43.21

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15	Lys A	la Asr 35	Gln	Gln	Lys	Gln	Asp 40	qeA	Gly	Arg	Gly	Leu 45	Val	Leu	Pro
	Gly T	yr Lys io	Tyr	Leu	Gly	Pro 55	Phe	Asn	Gly	Leu	Asp 60	Lys 	Gly	Glu	Pro
20	Val A 65	sn Ala	Ala	Asp	Ala 70.	Ala	Ala	Leu	Glu	His 75	Asp	Lys	Ala	Tyr	Asp 80
25		ln Leu		85					90					95	
. 30		la Glu	100					105					110		
30		eu Gly 115					120					125			
35	13	ly Leu 30				135					140				
40	145	al Glu			150					155					160
		nr Gly		165					170					175	
45		sp Ser	180					185					190		
50	Ala Al	195					200				:	205			
,	Ala Pr 21	.0	710	vah ,	W211	215	G I U	сту.	MIB .		220 220	val	era :	ASD.	ser

		Ser 225	-	aeA	Trp	His	Суя 230	_	Ser	Thr	Trp	Leu 235	-	Asp	Arg	Val	Ile 240
5		Thr	Thr	Ser	Thr	Arg 245		Trp	Ala	Leu	Pro 250		Tyr	Asn	neA	His 255	Leu
10		Tyr	Lys	Gln	Ile 260		Asn	Gly	Thr	Ser 265		Gly	Ser	Thr	Asn 270		Asn
		Thr	Tyr	Phe 275	Gly	Туг	Ser	Thr	Pro 280	_	Gly	Tyr	Phe	Asp 285		Asn	Arg
15		Phe	His 290	Cys	His	Phe	Ser	Pro 295	Arg	Asp	Trp	Gln	Arg 300	Leu	Ile	Asn	Asn
20		Asn 305	Trp	еју	Phe	Arg	Pro 310	Lys	Arg	Leu	Asn	Phe 315	Lys	Leu	Phe	Asn	Ile 320
		Gln	Val	Lys	Glu	Val 325	Thr	Thr	Asn	Glu	330 ela	Thr	ŗÀa	Thr	Ile	Ala 335	Asn
25		Asn	Leu	Thr	Ser 340	Thr	Val	Arg	Val	Phe 345	Thr	Asp	Ser	Glu	туг 350	Gln	Leu
30		Pro	Tyr	Val 355		Gly	Ser	Ala	His 360	Gln	Gly	Суз	Leu	Pro 365	Pro	Phe	Pro
05		Ala	Asp 370	Val	Phe	Met	Val	Pro 375	Gln	Tyr	Gly	Tyr	Leu 380	Thr	Leu	Asn	Asn
35		Gly 385	Ser	Gln	Ala	Leu	390	Arg	ser	Ser	Phe	Tyr 395	Суз	Leu	Glu	Tyr	Phe 400
40		Pro	Ser	Gln	Met	Leu 405	Arg	Thr	Gly	Asn	Asn 410	Phe	Gln	Phe	Ser	Tyr 415	Thr
		Phe	Glu	qzA	Val 420	Pro	Phe	His	Ser	Ser 425	Tyr	Ala	His	Ser	Gln 430	Ser	Leu
45		qeA	Arg	Leu 435	Met	Asn	Pro	Leu	Ile 440	Asp	Gln	Tyr	Leu	Tyr 445	Tyr	Leu	Val
50	:	Arg	Thr 450	Gln	Thr	Thr	Gly	Thr 455	Gly	Gly	Thr	Gln	Thr 460	Leu	Ala	Phe	Ser
		Gln 465	Ala	Gly	Pro	Ser	Ser 470	Met	Ala	Asn	Gln	Ala 475	Arg	Asn	Trp	Val	Pro 480
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		Gl	y Pr	o Cy	з Ту	r Ar 48		n Gl	n Ar	g Va	1 Se 49		r Th	r Th	ar As	3n Gl 49	
5		As	n As:	n Se	r As 50	n Ph O	e Al	a Tr	p Th	r G1 50		a Al	a Ly	's Ph	e Ly 51	s Le .0	u As:
10		Gly	y Ar	3 As 51	p Se 5	r Le	u Me	t As	n Pro 520	o G1	y Va	1 Al	a Me	t Al 52		r Hi	s Ly:
		Asp	Asr 530	As <sub>1</sub>	As <sub>1</sub>	p Ar	g Pho	e Ph 53	e Pro	Se	r Se	r Gl	y Va 54		u 'Il	e Ph	e Gly
15		Lys 545	Glr	. Gly	/ Ala	a Gly	y Ası 550	n As <sub>l</sub>	p Gly	/ Va.	l As	p Ty:		r Gl:	n Va	l Le	1 Ile 560
20		Thr	Asp	Glu	ı Glı	1 Glv 565	ı Ile	E Lys	a Ala	Thi	570	n Pro	Va.	l Ala	a Th	r Glv 575	
		Tyr	Gly	Ala	Val 580	. Ala	Ile	: Asr	Asn	Gl: 585		a Ala	Asz	Thi	590	n Ale	Gln
25		Thr	Gly	Leu 595	. Val	. His	Asn	Gln	Gly 600	Val	. Ile	Pro	Gly	/ Met 605		Trp	Gln
30	:	neA	Arg 610	Asp	Val	Tyr	Leu	Gln 615	Gly	Pro	Ile	Trp	Ala 620		Ile	Pro	His
		Thr 625	qeA	Gly	Asn	Phe	His 630	Pro	Ser	Pro	Leu	Met 635	Gly	Gly	Phe	Gly	Leu 640
35	ī	Lys	His	Pro	Pro	Pro 645	Gln	Ile	Leu	Ile	Lys 650		Thr	Pro	Val	Pro 655	Ala
40	3	qes	Pro	Pro	Leu 660	Thr	Phe	neA	Gln	Ala 665	Lys	Leu	Asn	Ser	Phe 670	Ile	Thr
	G	ln	Tyr	Ser 675	Thr	Gly	Gln	Val	Ser 680	Val	Glu	Ile	Glu	Trp 685	Glu	Leu	Gln
	L	ys	Glu 690	Asn	Ser	Lys	Arg	Trp 695	Asn	Pro	Glu	Ile	Gln 700	Tyr	Thr	Ser	Asn
50	T 7	yr 05	Tyr	Lys	Ser	Thr	Asn 710	Val	Asp	Phe	Ala	<b>Val</b> 715	Asn	Thr	Glu	Gly	Val 720
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<210> 97 <211> 736

<212> PRT <213> capsid protein of AAV serotype, clone 43.25

<400> 97

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15	Ly	s Al	a Ası 35	n Gln	Gln	Lys	Gl:	n Ası 40	eA q	p Gl	y Ar	g Gl	y Le	u Va	l Le	u Pro
	Gl	у Ту. 50	r Lys	туг	Leu	Gly	7 Pro	Phe	a Asr	, eJ	/ Let	Asp 60	Lys	G Gl	y Gl	u Pro
20	Va. 65	l Ası	n Ale	Ala	Asp	Ala 70	Ala	Ala	Lev	Glu	His 75	Asp	Lys	Ala	а ту:	r Asp 80
25					63					90					95	3 Ala
	•			Phe 100					105					110	1	
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35	Leu 	Gly 130	Leu	Val	Glu	Glu	Gly 135	Ala	Lys	Thr	Ala	Pro 140	Gly	Lys	Lys	Arg
	Pro 145	Val	Glu	Gln :	Ser	Pro 150	Gln	Glu	Pro	Asp	Ser 155	Ser	Ser	Gly	Ile	Gly 160
40	Lys	Thr	Gly	Gln (	3ln : 165	Pro	Ala	Lys	Lys	Arg 170	Leu	Asn	Phe	Gly	Gln 175	Thr
45	Gly	Asp	Ser	Glu S 180	er '	Val	Pro	Asp	Pro 185	Gln	Pro	Leu	Gly	Glu 190	Pro	Pro
	Ala	Ala	Pro 195	Ser G	ly I		Gly	Pro . 200	Asn '	Thr	Met .	Ala	Ser 205	Gly	Gly	Gly
50	Ala	Pro 210	Met i	Ala A	A qe.	usn i	Asn (	Glu (	Gly :	Ala :	qe <i>A</i>	51y ' 220	Val	ej y	Asn	Ser
ŧ	Ser 225	Gly	Asn 1	frp H	is C	ys ) 30	Asp :	Ser 7	Thr :	rp i	Leu ( 235	Sly X	Asp 2	Arg		Ile 240

		Thr	Thr	: Ser	Thr	Arg 245		Trp	Ala	Lev	250		Туг	ne.A	Asn	His 255	Leu		••	
5		Tyr	Lys	Gln	1le 260		Asn	Gly	Thr	ser 265		, e1?	, Ser	Thr	Asn 270		Asn			
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15		Phe	His 290		His	Phe	Ser	Pro 295	-	Asp	Trp	Gln	Arg 300		Ile	Asn	Asn			
		Asn 305		Gly	Phe	Arg	Pro 310	Lys	Arg	Leu	Asn	Phe 315	_	Leu	Phe	Asn	Ile 320	~		
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25		neA	Leu	Thr	Ser 340	Thr	Val	Gln	Val	Phe 345	Thr	Азр	Ser	Glu	Tyr 350	Gln	Leu			
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35		Gly 385		Gln	Ala	Leu	Gly 390	Arg	Ser	Ser	Phe	Tyr 395	Суз	Leu	Glu	Tyr	Phe 400			
•		Pro	Ser	Gln	Met	Leu 405	Arg	Thr	Gly	Asn	Asn 410	Phe	Gln	Phe	Ser	Tyr 415	Thr			
40		Phe	Glu	Asp	Val 420	Pro	Phe	His	Ser	Ser 425	Tyr	Ala	His	Ser	Gln 430		Leu-	-		
45				435		Asn			440					445	•				:	
		Arg	Thr 450	Gln	Thr	Thr	Gly	Thr 455	Gly	Gly	Thr	Gln	Thr 460	Leu	Ala	Phe	Ser			
50		465					470					475					480			
E E		Gly	Pro	Cys	Tyr	Arg 485	Gln	Gln	Arg	Val	Ser 490	Thr	Thr	Thr	Asn	<b>Gln</b> 495	Asn			

5		λ.	Sn A	sn S	er A. 50	sn Pi 00	ne A.	la T	cp T	hr G	ly A 05	la A	la L	ys P		ys L 10	eu Asn	
J		G.	ly Ai	rg As 51	sp Se	er Le	eu Me	et As	3n P. 5:	ro G 20	ly V	al A	la Me	et A 5	la S 25	er H:	is Lys	
10		As	p As 53	sp As 10	p As	p Ar	g Ph	ie Ph 53	e P:	ro S	er S	er G	Ly Va 54	l L	eu I	le Ph	e Gly	
15		Ly 54	's Gl 5	n Gl	y Al	a <b>Gl</b> ;	у Аз 55	eA n 0	E)	y V	al As	3p T) 55	r Se 55	r G	ln Va	al Le	u Ile 560	
		Th	r As	p Gl	u Gl	u Gli 565	u Il	e Ly	s Al	a Tì	ar As 57	n Pr	o Va	l al	la Th	ir Gl 57	u Glu 5	
20		<b>Ty</b> :	r Gl	y Al	580	l Ala	ı Ile	8 A31	eA n	n Gl 58	n Al 5	a Al	a Ası	n Th	r Gl 59		e Gln	
25		Thi	c Gl	y Let 595	ı Val	l His	Asr	Glr	60	y Va	1 11	e Pr	o Gly	у Ме 60	t Va 5	l Tr	Gln	
				٠				613	•				620	)			His	
30							050					633	•			e Gly	640	
<i>35</i>						015					650	)				655		
										665	•				670			
40	·· .								680					685		Leu		
15								025					700			Ser		
							710					715				Gly	720	
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<211> 736 <212> PRT

<213> capsid protein of AAV serotype, clone 43.23

<400> 98

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		Glı	ı Gly	y Ile	e Arg 20	Gl:	ı Tr	p Trp	geA o	Let 25	ı Ly:	s Pro	G1;	y Ala	a Pro	b Ly:	Pro
10		Ĺys	Ala	Asn 35	. Gln	Glr	l Lys	s Glr	Asp 40	qeA c	Gl)	y Arg	Gl <sub>3</sub>	y Let 45	ı Vai	l Lei	Pro
15		Gly	Tyr 50	Lys	Tyr	Leu	. Gly	Pro	Phe	Asn	Gly	Leu	Asp 60	Lys	Gl)	/ Glu	Pro
		Val 65	Asn	Ala	Ala	Asp	Ala 70	Ala	Ala	Leu	Glu	His 75	Asp	Lys	Ala	Tyr	Asp 80
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3 <i>5</i>		Pro 145	Val	Glu	Gln	Ser	Pro 150	Gln	Glu	Pro	qeA	Ser 155	Ser	Ser	Gly	Ile	Gly 160
		Lys	Thr	Gly	Gln	Gln 165	Pro	Ala	Lys	Lys	Arg 170	Leu	Asn	Phe	Gly	Gln 175	Thr
40		Gly	Asp	Ser	Glu 180	Ser	Val	Pro	qeA	Pro 185	Gln	Pro	Leu	Gly	Glu 190	Pro	Pro
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		Ala	Pro 210	Met .	Ala .	Asp	Asn	Asn 215	Glu	Gly.	Ala		Gly 220	Val	Gly	Asn	Ser
50	- ,	ser 225	Gly	Asn	Trp :	His	Cys 230	Asp	Ser	Thr		Leu ( 235	Gly	Asp	Arg		Ile 240

5 .	T	r Th	r Se	r Thi	24!	g Th	r Tr	p Al	a Le	u Pro 25		r Ty	c Ası	n Ası	n Hi 25	s Leu 5
	Τ)	r Ly:	s Gli	n Ile 260	e Sei	C As	n Gl	y Th	r Se. 26	r Gly 5	y Gl	y Sei	Thi	27(		neA q
10	Th	r Ty	275	e Gly	Туг	: Se	r Th	280	o Tri	e Gly	ту	Phe	285	Phe	As:	n Arg
15	Ph	e His 290	Cys	His	Phe	s Se	295	Arg	J Asp	Tr	Glr	300	Leu	Ile	: Ası	n Asn
	A.S. 30.	n Trp 5	Gly	Phe	Arg	9rc 310	Lys	Arg	Leu	Asn	Phe 315		Leu	Phe	Asr	320
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25	Ası	Leu	Thr	Ser 340	Thr	Val	Gln	Val	Phe 345	Thr	Ąsp	Leu	Glu	Tyr 350	e1v	Leu
	Pro	Tyr	Val 355	Leu	Gly	Ser	Ala	His 360	Gln	Gly	Суз	Leu	Pro 365	Pro	Phe	Pro
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	Phe	Glu	Asp	Val : 420	Pro	Phe	His	Ser	Ser 425	Tyr	Ala	His		Gln 430	Ser	Leu
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	Arg	Thr 450	Gln '	Thr 1	Thr (	3ly	Thr 455	Gly	Gly	Thr		Thr :				Ser
50	465	Ala	Gly :	Pro S	Ser S	Ser 470	Met .	Ala :	Asn (	Gln i	Ala 2 475	Arg 1	Asn 1	rp '		Pro 480
55	Gly	Pro (	Cys 1	Tyr A 4	rg (	-ln	Gln :	Arg '		Ser :	Chr :	Thr 7	Chr 7		3ln /	Asn

_		Asr	ne <i>A</i> r	ı Sei	500	Ph∈	e Ala	a Trp	Thi	50	y Ale 5	A Ala	a Lys	Phe	E Ly: 51		neA u
5		GJ À	/ Arg	7 Asp 515	Ser	Leu	ı Met	Asn	9rc 520		y Val	L Ala	a Met	325 525		Hi:	a Lys
10		Asp	Asp 530	Asp	n Asp	Arg	Ph€	Phe 535	Pro	Se	s Ser	: Gl	/ Val 540		ı Ile	e Phe	e Gly
15		Lys · 545	Gln	Gly	Ala	Gly	Asr 550		Gly	Va]	. Asp	7yr 555		Gln	(Va)	Le	1 Ile 560
13		Thr	Asp	Glu	Glu	Glu 565	Ile	Lys	Ala	Thr	370		Val	Ala	Thr	61u 575	Glu
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<i>2</i> 5		Thr	Gly	Leu 595	Val	His	Asn	Gln	Gly GOO	Val	Ile	Pro	Gly	Met 605	Val	Trp	Gln
		Asn	Arg 610	Asp	Val	Tyr	Leu	Gln 615	Gly	Pro	Ile	Trp	Ala 620	Lys	Ile	Pro	His
30		Thr 625	Asp	Gly	Asn	Phe	His 630	Pro	Ser	Pro	Leu	Met 635	Gly	Gly	Phe	Gly	Leu 640
<i>35</i>		Lys	His	Pro	Pro	Pro 645	Gln	Ile	Leu	Ile	Lys 650	Asn	Thr	Pro	Val	Pro 655	Ala
		Asp	Pro	Pro	Leu 660	Thr	Phe	Asn	Gln	Ala 665	Lys	Leu	Asn	Ser	Phe 670	Ile	Thr
40		Gln	Tyr	Ser 675	Thr	Gly	G1n	Val	Ser 680	Val	Glu	Ile	Glu	Trp 685	Glu	Leu	Gln
45		Lys	Glu 690	Asn	Ser	Lys	Arg	Trp 695	Asn	Pro	Glu	Ile	Gln 700	Tyr	Thr	Ser	neA
		Tyr 705	Tyr	Lys	Ser	Thr	Asn 710	Val	qeA	Phe	Ala	Val 715	Asn	Thr	Glu	Gly	Val 720
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<212> PRT

<213> capsid protein of AAV serotype, clone 43.20

<400>99

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10	ГЛЗ	Ala	Asn 35	Gln	Gln	ГÀЗ	Gln	Asp 40	qeA	Gly	Arg	Gly	Leu 45	Val	Leu	Pro
. 15	Gly	Tyr 50	Lys	Tyr	Leu	Gly	Pro 55	Phe	neA	Сlу	Leu	Asp 60	Lys	Gly	Glu	Pro
	Val 65	Asn	Ala	Ala	Asp	Ala 70	Ala	Ala	Leu	Glu	His 75	Asp	Lys	Ala	Tyr	Asp 80
20	Gln	Gln	Leu	Lys	Ala 85	Gly	Asp	Asn	Pro	Tyr 90	Leu	Arg	Tyr	Asn	His 95	Ala
25	Asp	Ala	Glu	Phe 100	Gln	Glu	Arg	Leu	Gln 105	Glu	qeA	Thr	Ser	Phe 110	СŢА	GЈУ
•	Asn	Leu	Gly 115	Arg	Ala	Val	Phe	Gln 120	Ala	Lys	Lys	Arg	Val 125	Leu	Glu	Pro
30	Leu	Gly 130	Leu	Val	Glu	Glu	Gly 135	Ala	Lys	Thr	Ala	Pro 140	Gly	Lys	Lys	Arg
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	Lys	Thr	Gly	Gln	Gln 165	Pro	Ala	Lys	Lys	Arg 170	Leu	Asn	Phe	Gly	Gln 175	Thr
40	Gly	Asp	Ser	Glu 180	Ser	Val	Pro	Asp	Pro 185	Gln	Pro	Leu	Gly	Glu 190	Pro	Pro
45	Ala	Ala	Pro 195	Ser	Gly	Leu	Gly	Pro 200	neA	Thr	Met	Ala	Ser 205	Gly	Gly	GJĀ
		Pro 210	Met	Ala	Asp	Asn	Asn 215	Glu	Gly	Ala	_	Gly 220	Val	Gly	Asn	Ser
50	Ser 225	ely	neA	Trp	His	Cys 230	Asp	Ser	Thr	Trp	Leu 235	Gly	Asp	Arg	Val	Ile 240

5		Thi	r Thu	r Se	r Thi	245	Thi	Tr	) Ala	a Lei	250		r Ty	I Ası	n Ası	n Hi 25.	
		Tyr	Lys	G Glr	1 Ile 260	e Ser	, Asr	Gly	/ Thi	2 65	c Gly	, el	y Se:	r Thi	270	n Ası	ne.A
10	٠	Thr	туг	275	e Gly	' Tyr	: Sez	Thr	280		ely	Ty:	Pho	285		e Ası	Arg
		Phe	His 290	Cys	His	Phe	ser	Pro 295	Arg	Asp	Trp	Glr	300		ılle	: Asr	Asn
15		Asn 305	Trp	Gly	Phe	Arg	Pro 310	Lys	Arg	Leu	neA ı	Phe 315		Leu	Phe	: Asr	11e 320
20		Gln	Val	Lys	Glu	Val 325	Thr	Thr	Asn	Glu	Gly 330	Thr	Lys	Thr	Ile	Ala 335	
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25		Pro	Tyr	Val 355	Leu	Gly	Ser	Ala	His 360	Gln	Gly	Cys	Leu	Pro 365	Pro	Phe	Pro
30		Ala	Asp 370	Val	Phe	Thr	Val	Pro 375	Gln	Tyr	Gly	Tyr	Leu 380	Thr	Leu	Asn	Asn
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		Asp	Arg	Leu 435	Met	Asn	Pro	Leu	Ile 440.		Gln	Tyr	Leu	Tyr 445	Tyr	Leu	Val
45		Arg	Thr 450	Gln	Thr	Thr	ela	Thr 455	Gly	GЉ	Thr	Gln	Thr 460	Leu	Ala	Phe	Ser
50		Gln 465	Ala	еĵà	Pro	Ser	Ser :	Met	Ala .	Asn		Ala 475	Arg	aeA	Trp	Val	Pro 480
	:	Gly	Pro	Cys		Arg 485	Gln	Gln .	Arg		Ser 490	Thr	Thr	Thr	Asn	Gln 495	Asn
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10		AŚp	Asp 530	Asp	qsA o	Arg	Phe	Phe 535	Pro	Ser	Ser	Gly	Val 540		Ile	Pbe	e Gly
15		Lys 545	Gln	Gly	Ala	Gly	Asn 550		Gly	Val	Asp	<b>Tyr</b> 555		Gln	Val	Leu	Tle 560
		Thr	Asp	Glu	Glu	Glu 565		Lys	Ala	Thr	Asn 570		Val	Ala	Thr	Glu 575	Glu
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23		Asn	Arg 610	Asp	Val	Tyr	Leu	Gln 615	Gly	Pro	Ile	Trp	Ala 620	Lys	Ile	Pro	His
30		Thr 625	Asp	Gly	Asn	Phe	His 630	Pro	Ser	Pro	Leu	Met 635	Gly	<b>G</b> Jy	Phe	Gly	Leu 640
35		Lys	His	Pro	Pro	Pro 645	Gln	Ile	Leu	Ile	Lys 650	Asn	Thr	Pro	Val	Pro 65S	Ala
		Asp	Pro	Pro	Leu 660	Thr	Phe	Asn	Gln	Ala 665	Lys	Leu	Asn	Ser	Phe 670	Ile	
40		Gln	Tyr	Ser 675	Thr	Gly	Gln	Val	ser 680	Val	Glu	Ile	Glu	Trp 685	Glu	Leu	Gln
45		Lys	Glu 690	Asn	Ser	Lys	Arg	Trp 695	Asn	Pro	Glu	Ile	Gln 700	Tyr	Thr	Ser	Asn
		Tyr 705	Tyr	Lys	Ser	Thr	Asn 710	Val	Asp	Phe	Ala	Val 715	aeA	Thr	Glu	Gly	Val 720
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	400> 100																

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5	G)/	ı Gly	y Ile	20	g Glu	Tr	Trp	reA o	Lev 25	Lys	Pro	61;	y Ala	a Pro	LY:	B Pro
10	Lys	ala	A Asr 35	Glr	Gln	Lys	Gln	40.	Asp	Gly	' Arg	eŢ	/ Let 45	ı Val	Lev	Pro
	G) y	7 Ty:	: Lys	Туг	Leu	Gly	Pro 55	Phe	neA:	Gly	Leu	A31 60	Lys	s Gly	Glu	Pro
15	Val 65	. Asn	Ala	Ala	· Asp	Ala 70	Ala	Ala	Leu	Glu	His 75	Asp	Lys	Ala	Tyr	qeA 08
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	qeA	Ala	Glu	Phe 100	Gln	Glu	Arg	Leu	Gln 105	Glu	Asp	Thr	Ser	Phe 110	Gly	Gly
25	Asn	Leu	Gly 115	Arg	Ala	Val	Phe	Gln 120	Äla	Lys	Lys	Arg	Val 125	Leu	Glu	Pro
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	Pro 145	Val	Glu	Gln	Ser	Pro 150	Gln	Glu	Pro	Asp	Ser 155	Ser	Ser	Gly	Ile	TeO GJÀ
35	Lys	Ser	Gly	Gln	Gln 165	Pro	Ala	Lys	Lys	Arg 170	Leu	Asn	Phe	Gly	Gln 175	Thr
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45	Ala	Pro 210	Met	Ala	Asp	neA	Asn 215	G) n	Gly	Ala	Asp	Gly 220	Val	Gly	Asn	Ser
50	Ser 225	Gly	Asn	Trp	His	Cys 230	Asp	Ser	Thr		Leu 235	Gly	qeA	Arg	Val	Ile 240
	·Thr	Thr	Ser	Thr	Arg 245	Thr	Trp .	Ala		Pro 250	Thr	Tyr	Asn		His 255	Leu

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	Thi	ту	275	e Gly	Y Tyz	Se	r Thi	280		p Gly	Ty:	r Phe	285		EA:	n Arg
10	Phe	His 290	cys	His	Phe	s Sei	295		l Yal	o Tr	Glr	Arg 300		lle	. Ası	asA ı
15	Asn 305	Trp	GJ7	Phe	Arg	9rc 310		Arg	Lei	neA ı	9he 315		Leu	Phe	Ası	1le 320
	Gln	Val	Lys	eln	Val 325	Thr	Thr	Asn	Glu	Gly 330	Thr	Lys	Thr	Ile	Ala 335	Asn
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25	Pro	Tyr	Val 355	Leu	Gly	Ser	Ala	His 360	Gln	Gly	Суз	Leu	Pro 365	Pro	Phe	Pro
	Ala	Asp 370	Val	Phe	Met	Val	Pro 375	Gln	Tyr	Gly	Tyr	Leu 380	Thr	Leu	Asn	Asn
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	Phe	Glu	Asp	Val 420	Pro	Phe	His	Ser	Ser 425	Tyr	Ala	His	Ser	Gln 430	Ser	Leu
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	Gln 465	Ala	Gly	Pro	Ser	Ser 470	Met .	Ala	Asn	Gln	Ala 475	Arg .	Asn	Trp	Val	Pro 480
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55	Asn .	Asn	Ser .	Asn 500	Phe .	Ala	Trp		Gly 505	Ala .	Ala	Lys		Lys : 510	Leu .	Asn

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		Ası	nes q Sec	o Glu	ı Ası	Arg	J Ph	e Phe 535	e Pro	Se	r Sei	Gl:	y Val 540	. Lei	ı Il	e Ph	e Gly
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		225					230					235				Ser	240
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20		Pro	610	_				615					620				
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	neA	ı Lev	115	Arg	Ala	. Val	Phe	Gln 120		Lys	Lys	Arg	Val 125		Gl:	Pro
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	Pr	o Le	u Ile 43	e Asp 5	Gln	Tyr	Lev	1 Ty:	т <b>Ту</b> :	r Lei	ı Ala	Arg	Thr 445		Ser	: Thr
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<b>4</b> 5		٠.		٠												

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.

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5				Let	1 Gl;	y Let 0	u Val	l Gl	u Gl	u Gl; 13	y Ala 5	a Ly:	s Th	r Al	a Pro		у Гу	s Ly:	a Arg
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#### 40 Claims

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- 1. A method of identifying unknown adeno-associated virus (AAV) sequences in a sample suspected of containing AAV from a latent infection, said method comprising the steps of:
  - (a) subjecting the sample containing DNA to amplification via polymerase chain reaction (PCR) using a first set of primers which specifically amplify a first AAV region comprising at least 250 bp of AAV capsid nucleic acid sequences, said first region having a variable sequence flanked by at least 18 base pairs of highly conserved sequence at its 5' end and at least 18 base pairs of highly conserved sequence at its 3' end, said base pairs being highly conserved relative to an alignment of at least AAV1, AAV2, AAV3, AAV4, AAV5 and AAV6;
    - (b) optionally subjecting the DNA to further amplification using a second set of primers which specifically amplify a second region which comprises the first region of AAV sequences and sequences which are 5' to the first region, such that AAV 5' extension sequences which anneal to the 5' end of the AAV sequences amplified by the primers for the first region are obtained;
    - (c) optionally subjecting the DNA to further amplification using a third set of primers which specifically amplify a third region which comprises the first region of AAV sequences and sequences which are 3' to the first region, such that AAV 3' extension sequences which anneal to the 3' end of the AAV sequences amplified by the primers for the first region are obtained,

each of said second and third regions being predetermined based upon the alignment of the nucleic acid sequences of at least AAV1, AAV2, AAV3. AAV4, AAV5 and AAV6, and each of said regions comprising nucleic acid sequences which are highly conserved over at least 18 base pairs at the 5' end, optionally variable sequences in the middle, and sequences which are highly conserved over at least 18 base pairs at the 3' end of the sequences of the region, relative to the sequences of at least AAV1, AAV2, AAV3, AAV4, AAV5 and AAV6; and each of the sets of primers consisting of a 5' primer and a 3' primer; the presence of amplified sequences indicating the presence of an AAV in the sample, and a comparison of differences between the amplified sequences and the sequences of AAV1, AAV2, AAV3, AAV4, AAV5 and AAV6 indicating the presence of an unknown AAV.

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2. A method according to claim 1, wherein the comparison comprises the step of comparing restriction enzyme patterns for the amplified sequences to restriction enzyme patterns of AAV1, AAV2, AAV3, AAV4, AAV5 and AAV6.

3. A method according to claim 1 or claim 2, wherein step (a) amplifies the full-length capsid gene.

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4. A method according to any of claims 1 to 3, wherein the amplified sequences comprise the AAV capsid gene and the AAV rep gene.

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5. A method according to any of claims 1 to 4, wherein the DNA has been extracted from cells, cell culture, tissue, tissue culture or biological fluids.

6. A method according to any of claims 1 to 5, wherein the first region is highly conserved over at least about 25 base pairs at the 5' end of the region, the 3' end of the region or both.

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7. A method according to claim 6, wherein the first region is highly conserved over at least about 30 base pairs at the 5' end of the region, the 3' end of the region or both.

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8. A method according to any of claims 1 to 7, wherein the highly conserved sequences of the first region have at least 80% identity among the aligned AAVs at the 5' end of the region, the 3' end of the region or both.

A method according to claim 8, wherein the highly conserved sequences of the first region have at least 90% identity
among the aligned AAVs at the 5' end of the region, the 3' end of the region or both.

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10. A method according to any of claims 1 to 9, wherein the variable sequences in the middle of the first region have less than 70% identity among the aligned AAVs.

11. A method according to any of claims 1 to 10, wherein the first region spans about bp 2800 to about 3200 of AAV 1, SEQ ID NO:6, and corresponding base pairs in other AAVs.

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12. A method according to claim 11, wherein the first region is 257 bp spanning bp 2886 to about 3143 of AAV 1, SEQ ID NO:6, and corresponding base pairs in other AAVs.

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13. A method according to any of claims 1 to 5, wherein the primers axe AV1ns, having the sequence ofnncieotides 1398 to 1423 of SEQ ID NO:6. and AV2cas, having the sequence of SEQ ID NO:7.

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14. A method according to claim 1 or claim 2, wherein the first set of primers allows isolation of full-length adeno-associated virus capsid sequences from a sample, the first set of primers comprising a 5' primer directed to a region located in the middle of an AAV rep gene, based on a predetermined conserved region, and a 3' primer directed to a region downstream of an AAV cap gene, based on a predetermined conserved region of AAV.

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15. A method according to any of claims 1 to 14, wherein the sample comprises AAV integrated into the chromosome.

16. A method according to any of claims 1 to 15, wherein the sample comprises human tissue.

- 17. A method according to any of claims 1 to 16, wherein the sample contains proviral AAV sequences.
- 18. A method according to any of claims 1 to 17, wherein the first region is a signature region.

- 19. A method according to any of claims 1 to 18, wherein the base pairs of the highly conserved sequences are highly conserved relative to an alignment of AAVs 1,2,3,4,5 and 6 and AAVs isolated from geese and ducks.
- 20. A method according to any of claims 1 to 19, wherein the variable sequence is a hypervariable sequence.

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- 21. A method according to any of claims 1 to 20, wherein the first region comprises up to 10 kilobasepairs in length.
- 22. A method according to claim 21, wherein the first region comprises a 3-1 kilobase pair fragment comprising the full-length cap sequence.
- 23. A kit for detecting the presence of an unknown adeno-associated virus (AAV) in a sample from cellular DNA suspected of containing a latent AAV infection, said kit comprising:
  - (a) a first set of primers which specifically amplify a first region comprising 250 bp of AAV capsid nucleic acid sequences, said first region having at least 18 base pairs of highly conserved sequence at its 5' end, a variable sequence, and at least 18 base pairs of highly conserved sequence at its 3' end, said base pairs being highly conserved relative to an alignment of at least AAV1, AAV2, AAV3, AAV4, AAV5 and AAV6;
  - (b) optionally a second set of primers specific for a second region of the AAV nucleic acid sequences which comprises the first region of AAV sequences and sequences which are 5' to the first region, such that AAV 5' extension sequences which anneal to the 5' end of the AAV sequences amplified by the primers for the first region are obtained;
  - (c) optionally a third set of primers which specifically amplify a third region which comprises the first region of AAV sequences and sequences which are 3' to the first region, such that AAV 3' extension sequences which anneal to the 3' end of the AAV sequences amplified by the primers for the first region are obtained;

each of said second and third regions being predetermined based upon the alignment of the nucleic acid sequences of at least AAV1, AAV2, AAV3, AAV4, AAV5 and AAV6, and each of said regions comprising nucleic acid sequences which are highly conserved over at least 18 base pairs at the 5' end, optionally variable sequences in the middle, and sequences which are highly conserved over at least 18 base pairs at the 3' end of the sequences of the region, relative to the sequences of at least AAV1, AAV2, AAV3, AAV4, AAV5 and AAV6; each of the sets of primers consisting of a 5' primer and a 3' primer, each of said primers comprising at least 15 nucleotides complementary to its respective highly conserved sequence and having exact identity with its respective highly conserved sequence over at least 5 base pairs in its 3' end.

- 24. A kit according to claim 23, wherein the 5' primer and/or the 3' primer comprises at least 18 nucleotides.
  - 25. A kit according to claim 24, wherein the 5' primer and/or the 3' primer comprises 25 nucleotides.
- 26. A kit according to any of claims 23 to 25, wherein the 5' primer and/or the 3' primer comprises at least 9 base pairs of exact identity at its 3' end.
  - 27. A kit according to claim 26, wherein the 5' primer and/or the 3' primer comprises at least 18 base pairs of exact identity at its 3' end.
- 28. A kit according to any of claims 23 to 27, wherein the first set of primers allows isolation of full-length adeno-associated virus capsid sequences from a sample, the first set of primers comprising a 5' primer directed to a region located in the middle of an AAV rep gene, based on a predetermined conserved region of AAV, and a 3' primer directed to a region downstream of an AAV cap gene, based on a predetermined conserved region of AAV.
  - 29. A kit according to claim 23, wherein the 5' primer has a sequence comprising GCTGCGTCAACTGGACCAATGA-GAA'C, which corresponds to nt 1398 to 1423 of SEQ ID NO:6.
- 30. A kit according to claim 23, wherein the 3' primer has a sequence comprising CGCAGAGACCAAAGTTCAACT 55 GAAACGA, which corresponds to the nucleotides complementary to 4462-4435 of SEQ ID NO:7.
  - 31. A kit according to any of claims 23 to 30, wherein the sample comprises AAV integrated into the chromosome.

#### Patentansprüche

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- Verfahren zur Identifizierung unbekannter Sequenzen von adeno-assoziiertem Virus (AAV) in einer Probe, von der man annimmt, daß sie von einer latenten Infektion herrührendes AAV enthält, wobei man in den folgenden Verfahrenschritten
  - (a) die DNA-haltige Probe einer Amplifikation über eine Polymerasekettenreaktion (PCR) unter Verwendung eines ersten Primersatzes, mit dem spezifisch ein mindestens 250 Bp AAV-Capsid-Nukleinsäuresequenzen umfassender erster AAV-Bereich amplifiziert wird, wobei dieser erste Bereich eine an ihrem 5'-Ende von mindestens 18 Basenpaaren hochkonservierter Sequenz und an ihrem 3'-Ende von mindestens 18 Basenpaaren hochkonservierter Sequenz aufweist, wobei die Basenpaare relativ zu einer vergleichenden Anordnung von mindestens AAV1, AAV2, AAV3, AAV4, AAV5 und AAV6 hochkonserviert sind, aussetzt,
  - (b) gegebenenfalls die DNA einer weiteren Amplifikation unter Verwendung eines zweiten Primersatzes, mit dem spezifisch ein zweiter Bereich, der den ersten Bereich von AAV-Sequenzen sowie 5' zum ersten Bereich liegende Sequenzen umfaßt, amplifiziert wird, aussetzt, so daß 5'-AAV-Verlängerungssequenzen, die in einer Annealing-Reaktion an das 5'-Ende der mit den Primern für den ersten Bereich amplifizierten AAV-Sequenzen binden, erhalten werden.
  - (c) gegebenenfalls die DNA einer weiteren Amplifikation unter Verwendung eines dritten Primersatzes, mit dem spezifisch ein dritter Bereich, der den ersten Bereich von AAV-Sequenzen sowie 3' zum ersten Bereich liegende Sequenzen umfaßt, amplifiziert wird, aussetzt, so daß 3'-AAV-Verlängerungssequenzen, die in einer Annealing-Reaktion an das 3'-Ende der mit den Primern für den ersten Bereich amplifizierten AAV-Sequenzen binden, erhalten werden,
- wobei der zweite und der dritte Bereich jeweils auf der Grundlage der vergleichenden Anordnung der Nukleinsäuresequenzen von mindestens AAV1, AAV2, AAV3, AAV4, AAV5 und AAV6 vorbestimmt sind und die Bereiche relativ zu den Sequenzen von mindestens AAV1, AAV2, AAV3, AAV4, AAV5 und AAV6 jeweils am 5'-Ende der Sequenzen des Bereichs über mindestens 18 Basenpaare hochkonservierte Nukleinsäuresequenzen, in der Mitte gegebenenfalls variable Sequenzen und am 3'-Ende über mindestens 18 Basenpaare hochkonservierte Sequenzen umfassen und
  - die Primersätze jeweils aus einem 5'-Primer und einem 3'-Primer bestehen, das Vorhandensein amplifizierter Sequenzen das Vorhandensein eines AAV in der Probe anzeigt, und ein Vergleich der Unterschiede zwischen den amplifizierten Sequenzen und den Sequenzen von AAV1, AAV2, AAV3, AAV4, AAV5 und AAV6 das Vorhandensein eines unbekannten AAV anzeigt.
  - Verfahren nach Anspruch 1, wobei der Vergleich den Schritt des Vergleichens von Restriktionsenzymmustern für die amplifizierten Sequenzen mit Restriktionsenzymmustern von AAV1, AAV2, AAV3, AAV4, AAV5 und AAV6 umfaßt.
- 40 3. Verfahren nach Anspruch 1 oder 2, wobei in Schritt (a) das Capsid-Gen in voller Länge amplifiziert wird.
  - 4. Verfahren nach einem der Ansprüche 1 bis 3, wobei die amplifizierten Sequenzen das AAV-Capsid-Gen und das AAV-rep-Gen umfassen.
- Verfahren nach einem der Ansprüche 1 bis 4, wobei die DNA aus Zellen, Zellkultur, Gewebe, Gewebekultur oder biologischen Flüssigkeiten extrahiert wurde.
  - Verfahren nach einem der Ansprüche 1 bis 5, wobei der erste Bereich über mindestens etwa 25 Basenpaare am 5'-Ende oder/und am 3'-Ende des Bereichs hochkonserviert ist.
  - 7. Verfahren nach Anspruch 6, wobei der erste Bereich über mindestens etwa 30 Basenpaare am 5'-Ende oder/und am 3'-Ende des Bereichs hochkonserviert ist.
- Verfahren nach einem der Ansprüche 1 bis 7, wobei die hochkonservierten Sequenzen des ersten Bereichs unter den vergleichend angeordneten AAVs eine Identität von mindestens 80% am 5'-Ende oder/und am 3'-Ende des Bereichs aufweisen.
  - 9. Verfahren nach Anspruch 8, wobei die hochkonservierten Sequenzen des ersten Bereichs unter den vergleichend

angeordneten AAVs eine Identität von mindestens 90% am 5'-Ende oder/und am 3'-Ende des Bereichs aufweisen.

- 10. Verfahren nach einem der Ansprüche 1 bis 9, wobei die variablen Sequenzen in der Mitte des ersten Bereichs unter den vergleichend angeordneten AAVs eine Identität von weniger als 70% aufweisen.
- 11. Verfahren nach einem der Ansprüche 1 bis 10, wobei der erste Bereich von etwa Bp 2800 bis etwa 3200 von AAV1, SEQ ID NO:6, und den entsprechenden Basenpaaren in anderen AAV reicht.
- 12. Verfahren nach Anspruch 11, wobei es sich bei dem ersten Bereich um 257 Bp handelt, die von Bp 2886 bis etwa
   3143 von AAV1, SEQ ID NO:6, und den entsprechenden Basenpaaren in anderen AAV reichen.
  - 13. Verfahren nach einem der Ansprüche 1 bis 5, wobei es sich bei den Primern um AV1ns mit der Sequenz der Nukleotide 1398 bis 1423 der SEQ ID NO:6 sowie um AV2cas mit der Sequenz der SEQ ID NO:7 handelt.
- 15 14. Verfahren nach Anspruch 1 oder Anspruch 2, wobei der erste Primersatz die Isolierung von Capsidsequenzen in voller L\u00e4nge von adeno-assoziiertem Virus aus einer Probe gestattet, wobei der erste Primersatz einen auf einen in der Mitte eines AAV-rep-Gens liegenden Bereich auf der Grundlage eines vorbestimmten konservierten Bereichs gerichteten 5'-Primer sowie einen auf einen stromabw\u00e4rts von einem AAV-cap-Gen liegenden Bereich auf der Grundlage eines vorbestimmten konservierten Bereichs von AAV gerichteten 3'-Primer umfa\u00dfts.
  - 15. Verfahren nach einem der Ansprüche 1 bis 14, wobei die Probe in das Chromosom integriertes AAV umfaßt.
  - 16. Verfahren nach einem der Ansprüche 1 bis 15, wobei die Probe menschliches Gewebe umfaßt.
  - 17. Verfahren nach einem der Ansprüche 1 bis 16, wobei die Probe provirale AAV-Sequenzen enthält.
  - 18. Verfahren nach einem der Ansprüche 1 bis 17, wobei es sich bei dem ersten Bereich um einen Signaturbereich handelt.
  - 19. Verfahren nach einem der Ansprüche 1 bis 18, wobei die Basenpaare der hochkonservierten Sequenzen relativ zu einer vergleichenden Anordnung von AAV 1, 2, 3, 4, 5 und 6 und aus Gans und Ente isolierten AAV hochkonserviert sind.
- 20. Verfahren nach einem der Ansprüche 1 bis 19, wobei es sich bei der variablen Sequenz um eine hypervariable Sequenz handelt.
  - Verfahren nach einem der Ansprüche 1 bis 20, wobei der erste Bereich eine Länge von bis zu 10 Kilobasenpaaren umfaßt.
  - 22. Verfahren nach Anspruch 21, wobei der erste Bereich ein die cap-Sequenz in voller Länge umfassendes Fragment von 3,1 Kilobasenpaaren umfaßt.
- 23. Kit zum Nachweis des Vorhandenseins eines unbekannten adeno-assoziierten Virus (AAV) in einer Probe aus zellulärer DNA, von der man annimmt, daß sie eine latente AAV-Infektion enthält, wobei der Kit umfaßt:
  - (a) einen ersten Primersatz, mit dem spezifisch ein 250 Bp AAV-Capsid-Nukleinsäuresequenzen umfassender erster AAV-Bereich amplifiziert wird, wobei dieser erste Bereich an seinem. 5'-Ende mindestens 18 Basenpaare hochkonservierter Sequenz, eine variable Sequenz und an seinem 3'-Ende mindestens 18 Basenpaare hochkonservierter Sequenz aufweist, wobei die Basenpaare relativ zu einer vergleichenden Anordnung von mindestens AAV1, AAV2, AAV3, AAV4, AAV5 und AAV6 hochkonserviert sind,
  - (b) gegebenenfalls einen für einen zweiten Bereich der AAV-Nukleinsäuresequenzen, der den ersten Bereich von AAV-Sequenzen sowie 5' zum ersten Bereich liegende Sequenzen umfaßt, spezifischen zweiten Primersatz, so daß 5'-AAV-Verlängerungssequenzen, die in einer Annealing-Reaktion an das 5'-Ende der mit den Primern für den ersten Bereich amplifizierten AAV-Sequenzen binden, erhalten werden.
  - (c) gegebenenfalls einen dritten Primersatz, mit dem spezifisch ein dritter Bereich, der den ersten Bereich von AAV-Sequenzen sowie 3' zum ersten Bereich liegende Sequenzen umfaßt, amplifiziert wird, so daß 3'-AAV-Verlängerungssequenzen, die in einer Annealing-Reaktion an das 3'-Ende der mit den Primern für den ersten

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Bereich amplifizierten AAV-Sequenzen binden, erhalten werden,

wobei der zweite und der dritte Bereich jeweils auf der Grundlage der vergleichenden Anordnung der Nukleinsäuresequenzen von mindestens AAV1, AAV2, AAV3, AAV4, AAV5 und AAV6 vorbestimmt sind und die Bereiche relativ zu den Sequenzen von mindestens AAV1, AAV2, AAV3, AAV4, AAV5 und AAV6 jeweils am 5'-Ende der Sequenzen des Bereichs über mindestens 18 Basenpaare hochkonservierte Nukleinsäuresequenzen, in der Mitte gegebenenfalls variable Sequenzen und am 3'-Ende über mindestens 18 Basenpaare hochkonservierte Sequenzen umfassen,

die Primersätze jeweils aus einem 5'-Primer und einem 3'-Primer bestehen, wobei jeder Primer mindestens 15 zur hochkonservierten Sequenz des jeweils anderen Primers komplementäre Nukleotide umfaßt und an seinem 3'-Ende über mindestens 5 Basenpaare eine genaue Identität mit der hochkonservierten Sequenz des jeweils anderen Primers aufweist.

- 24. Kit nach Anspruch 23, wobei der 5'-Primer und/oder der 3'-Primer mindestens 18 Nukleotide umfaßt.
- 25. Kit nach Anspruch 24, wobei der 5'-Primer und/oder der 3'-Primer mindestens 25 Nukleotide umfaßt.
- 26. Kit nach einem der Ansprüche 23 bis 25, wobei der 5'-Primer und/oder der 3'-Primer an seinem 3'-Ende mindestens 9 Basenpaare genauer Identität umfaßt.
- 27. Kit nach Anspruch 26, wobei der 5'-Primer und/oder der 3'-Primer an seinem 3'-Ende mindestens 18 Basenpaare genauer Identität umfaßt.
- 28. Kit nach einem der Ansprüche 23 bis 27, wobei der erste Primersatz die Isolierung von Capsidsequenzen in voller Länge von adeno-assoziiertem Virus aus einer Probe gestattet, wobei der erste Primersatz einen auf einen in der Mitte eines AAV-rep-Gens liegenden Bereich auf der Grundlage eines vorbestimmten konservierten Bereichs von AAV gerichteten 5'-Primer sowie einen auf einen stromabwärts von einem AAV-cap-Gen liegenden Bereich auf der Grundlage eines vorbestimmten konservierten Bereichs von AAV gerichteten 5'-Primer umfaßt.
  - 29. Kit nach Anspruch 23, wobei der 5'-Primer eine GCTGCGTCAACTGGACCAATGAGAAC umfassende Sequenz aufweist, die Nt 1398 bis 1423 der SEQ ID NO:6 entspricht.
  - 30. Kit nach Anspruch 23, wobei der 3'-Primer eine CGCAGAGACCAAAGTTCAACTGAAACGA umfassende Sequenz aufweist, die den zu 4462-4435 der SEQ ID NO:7 komplementären Nukleotiden entspricht.
    - 31. Kit nach einem der Ansprüche 23 bis 30, wobei die Probe in das Chromosom integriertes AAV umfaßt.

#### 40 Revendications

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- Procèdé pour identifier des séquences de virus associés à l'adénovirus (VAA) inconnus dans un échantillon dont on suspecte qu'il contient des VAA provenant d'une infection latente, ledit procèdé comprenant les étapes :
- (a) de soumission de l'échantillon contenant l'ADN à une amplification via une réaction de polymérase en chaîne (PCR) en utilisant une première série d'amorces qui amplifient spécifiquement une première région de VAA comprenant au moins 250 pb des séquences d'acides nucléiques de capside de VAA, ladite première région présentant une séquence variable adjacente à au moins 18 paires de bases d'une séquence hautement conservée en son extrémité 5' et à au moins 18 paires de bases d'une sèquence hautement conservée en son extrémité 3', lesdites paires de bases étant hautement conservées par rapport à un alignement d'au moins VAA1, VAA2, VAA3, VAA4, VAA5 et VAA6;
  - (b) éventuellement de soumission de l'ADN à une autre amplification en utilisant une deuxième série d'amorces qui amplifient spécifiquement une deuxième région qui comprend la première région de séquences des VAA et des séquences qui sont côté 5' par rapport à la première région, de telle manière qu'on obtient des séquences d'extension 5' de VAA qui hybrident sur l'extrémité 5' des séquences de VAA amplifiées par les amorces pour la première région ;
  - (c) éventuellement de soumission de l'ADN à une autre amplification utilisant une troisième série d'amorces qui amplifient spécifiquement une troisième région qui comprend la première région de séquences de VAA et

les séquences qui sont situées côté 3' par rapport à la première région, de telle manière qu'on obtient des séquences d'extension 3' de VAA qui hybrident sur l'extrémité 3' des séquences de VAA amplifiées par les amorces pour la première région,

chacune desdites deuxième et troisième régions étant prédéterminée sur base de l'alignement des séquences d'acides nucléiques d'au moins VAA1, VAA2, VAA3, VAA4, VAA5 et VAA6, et chacune desdites régions comprenant des séquences d'acides nucléiques qui sont hautement conservées sur au moins 18 paires de bases en l'extrémité 5', des séquences éventuellement variables au centre et des séquences qui sont hautement conservées sur au moins 18 paires de bases en l'extrémité 3' des séquences de la région, par rapport aux séquences d'au moins VAA1, VAA2, VAA3, VAA4, VAA5 et VAA6; et

chacune des séries d'amorces étant constituée par une amorce 5' et une amorce 3'; la présence de séquences amplifiées indiquant la présence d'un VAA dans l'échantillon et une comparaison des différences entre les séquences amplifiées et les séquences des VAA1, VAA2, VAA3, VAA4, VAA5 et VAA6 indiquant la présence d'un VAA inconnu.

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- Procédé selon la revendication 1, dans lequel la comparaison comprend l'étape de comparaison de modèles d'enzymes de restriction pour les séquences amplifiées à des modèles d'enzymes de restriction des VAA1, VAA2, VAA3, VAA4, VAA5 et VAA6.
- 20 3. Procédé selon la revendication 1 ou 2, dans lequel l'étape (a) amplifie toute 1a longueur du gène cap.
  - 4. Procède selon l'une quelconque des revendications 1 à 3, dans lequel les séquences amplifiées comprennent le gène cap du VAA et le gène rep du VAA.
- Procédé selon l'une quelconque des revendications 1 à 4, dans lequel l'ADN a été extrait de cellules, d'une culture cellulaire, de tissu, d'une culture de tissu ou de fluides biologiques.
  - 6. Procédé selon l'une quelconque des revendications 1 à 5, dans lequel la première région est hautement conservée sur au moins 25 paires de base en l'extrémité 5' de la région, en l'extrémité 3' de la région ou les deux.

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- 7. Procédé selon la revendication 6, dans lequel la première région est hautement conservée sur au moins 30 paires de base en l'extrèmité 5' de la région, en l'extrémité 3' de la région ou les deux.
- 8. Procédé selon l'une quelconque des revendications 1 à 7, dans lequel les séquences hautement conservées de la première région présentent une identité d'au moins 80% avec les VAA alignés en l'extrémité 5' de la région, l'extrémité 3' de la région ou les deux.
  - 9. Procèdé selon la revendication 8, dans lequel les séquences hautement conservées de la première région présentent une identité d'au moins 90% avec les VAA alignés en l'extrémité 5' de la région, l'extrémité 3' de la région ou les deux.

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10. Procédé selon l'une quelconque des revendications 1 à 9, dans lequel les séquences variables au centre de la première région présentent une identité inférieure à 70% avec les VAA alignés.

11. Procédé selon l'une quelconque des revendications 1 à 10, dans lequel la première région s'étend de la paire de bases 2800 à environ 3200 du VAA 1, SEQ ID NO:6, et les paires de bases correspondantes dans les autres VAA.

12. Procédé selon la revendication 11, dans lequel la première région représente 257 paires de bases, s'étendant de la paire de bases 2886 à environ 3143 du VAA1, SEQ ID NO:6, et les paires de bases correspondantes dans les autres VAA.

- 13. Procèdé selon l'une quelconque des revendications 1 à 5, dans lequel les amorces sont des AV1ns, présentant la séquence des nuclèotides 1398 à 1423 de la SEQ ID NO:6, et des AV2cas, présentant la séquence de la SEQ ID NO:7.
- 14. Procédé selon la revendication 1 ou 2, dans lequel la première série d'amorces permet l'isolement de toute la longueur de séquences de capside du virus associé à l'adénovirus d'un échantillon, la première série d'amorces comprenant une amorce 5' dirigée sur une région localisée au centre d'un gène rep du VAA, sur base d'une région prédéterminée conservée et une amorce 3', dirigée sur une région en avai d'un gène cap du VAA, basée sur une

règion prédéterminée conservée du VAA.

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- 15. Procédé selon l'une quelconque des revendications 1 à 14, dans lequel l'échantillon comprend un VAA intégré dans le chromosome.
- 16. Procédé selon l'une quelconque des revendications 1 à 15, dans lequel l'échantillon comprend du tissu humain.
- 17. Procédé selon l'une quelconque des revendications 1 à 16, dans lequel l'échantillon contient des sèquences de VAA provirales.
- 18. Procédé selon l'une quelconque des revendications 1 à 17, dans lequel la première région est une région de signature.
- 19. Procédé selon l'une quelconque des revendications 1 à 18, dans lequel les paires de bases des séquences hautement conservées sont hautement conservées par rapport à un alignement des VAA 1,2,3,4,5 et 6 et des VAA isolés à partir d'oies et de canards.
- 20. Procédé selon l'une quelconque des revendications 1 à 19, dans lequel la séquence variable est une séquence hypervariable.
- 20 21. Procédé selon l'une quelconque des revendications 1 à 20, dans lequel la première région comprend jusqu'à 10 kilopaires de bases en longueur.
  - 22. Procédé selon la revendication 21, dans lequel la première région comprend un fragment de 3,1 kilopaires de bases comprenant toute la longueur de la séquence du capside.
  - 23. Kit pour détecter la présence d'un virus associé à l'adénovirus (VAA) inconnu dans un échantillon d'ADN cellulaire dont on suspecte qu'il contient une infection latente par un VAA, ledit kit comprenant:
    - (a) une première série d'amorces qui amplifient spécifiquement une première région comprenant 250 paires de bases de séquences d'acides nucléiques d'un capside de VAA, ladite première région présentant au moins 18 paires de bases d'une séquence hautement conservée en son extrémité 5', une séquence variable et au moins 18 paires de base d'une séquence hautement conservée en son extrémité 3', lesdites paires de bases étant hautement conservées par rapport à un alignement d'au moins VAA1, VAA2, VAA3, VAA4, VAA5 et VAA6; (b) éventuellement une deuxième série d'amorces spécifiques d'une deuxième région des séquences d'acides nucléiques de VAA qui comprend la première région des séquences de VAA et des séquences qui se situent côté 5' par rapport à la première région, de manière à obtenir des séquences d'extension 5' des VAA qui hybrident sur l'extrémité 5' des séquences de VAA amplifient spécifiquement une troisième région, qui comprend la première région de séquences de VAA et des séquences qui se situent côté 3' par rapport à la première région, de manière à obtenir des séquences de VAA et des séquences qui se situent côté 3' par rapport à la première région, de manière à obtenir des séquences d'extension 3' de VAA qui hybrident sur l'extrémité 3' des séquences
    - chacune desdites deuxième et troisième région étant prédéterminée sur base de l'alignement des séquences d'acides nucléiques d'au moins les VAA1, VAA2, VAA3, VAA4, VAA5 et VAA6, et chacune desdites régions comprenant des séquences d'acides nucléiques qui sont hautement conservées sur au moins 18 paires de bases en l'extrémité 5', éventuellement des séquences variables au centre et des séquences qui sont hautement conservées sur au moins 18 paires de bases en l'extrémité 3' des séquences de la région, par rapport aux séquences au moins des VAA1, VAA2, VAA3, VAA4, VAA5 et VAA6;
    - chacune des séries d'amorces étant constituée par une amorce 5' et une amorce 3', chacune desdites amorces comprenant au moins 15 nucléotides complémentaires à sa séquence respective hautement conservée et présentant une identité exacte avec sa séquence respective hautement conservée sur au moins 5 paires de bases en son extrémité 3'.
  - 24. Kit selon la revendication 23, dans lequel l'amorce 5' et/ou l'amorce 3' comprend au moins 18 nucléotides.
  - 25. Kit selon la revendication 24, dans lequel l'amorce 5' et/ou l'amorce 3' comprend 25 nucléotides.

de VAA amplifiées par les amorces de la première région;

26. Kit selon l'une quelconque des revendications 23 à 25, dans lequel l'amorce 5' et/ou l'amorce 3' comprend au moins

9 paires de bases d'identité exacte en son extrémité 3'.

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- 27. Kit selon la revendication 26, dans lequel l'amorce 5' et/ou l'amorce 3' comprend au moins 18 paires de bases d'identité exacte en son extrémité 3'.
- 28. Kit selon l'une quelconque des revendications 23 à 27, dans lequel la première série d'amorces permet l'isolement de toute la longueur des séquences de capside d'un virus associé à l'adénovirus d'un échantillon, la première série d'amorces comprenant une amorce 5' dirigée sur une région localisée au centre d'un gène rep d'un VAA, basée sur une région prédéterminée conservée d'un VAA et une amorce 3' dirigée sur une région en aval d'un gène cap d'un VAA, basée sur une région prédéterminée conservée d'un VAA.
- 29. Kit selon 1a revendication 23, dans lequel l'amorce 5' présente une séquence comprenant GCTGCGTCAACTG-GACCAATGAGAAC, ce qui correspond aux nucléotides 1398 à 1423 de la SEQ ID NO:6.
- 30. Kit selon la revendication 23, dans lequel l'amorce 3' présente une séquence comprenant CGCAGAGACCAAAGTT-CAACTGAAACGA, qui correspond aux nucléotides complémentaires à 4462-4435 de la SEQ ID NO:7.
  - 31. Kit selon l'une quelconque des revendications 23 à 30, dans lequel l'échantillon comprend un VAA intégré dans le chromosome.